3348, Ap 3564, Ap 461, Ap 461, Ap 1627, Ap 2208, Ap 11583, Ap 11393, Ap 11393, Ap 11393, Ap 11393, Ap 11393, Ap 11062, Ap 11062, Ap 1164, Ap 1164, Ap 2206, Ap 2206, Ap 221, App 221, A

Sequence 1 Sequence 1 Sequence 1

Sequence

Sequence 5 Sequence 5 Sequence 3

Sequence Sequence Sequence

Sequence Sequence

Sequence Sequence Sequence Sequence

Sequence 3 Sequence 5 Sequence 5

Sequence:

Run on:

Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence

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Sequence 355, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
GIL H. Choi
Patrick S. Dillon
Craig A. Rosen
Fisher C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
STREET: 9410 Key West Avenue
STREET: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33

OPERALING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-0ct-1997
CLASSIFICATION ONTA: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
US-09-710-279-3348

US-09-710-279-4042

US-09-543-681A-2690

US-09-543-681A-2690

US-09-902-540-2208

US-09-902-540-2208

US-09-902-540-1583

US-09-902-540-1583

US-09-902-540-1583

US-09-134-000C-937

US-09-134-000C-937

US-09-134-000C-937

US-09-134-000C-2023

US-09-134-000C-2023

US-09-134-000C-2023

US-09-134-000C-2023

US-09-134-000C-2023

US-09-134-110-1062

US-09-131-127-164

US-09-131-127-164

US-09-131-1312

US-09-131-13116

US-09-107-133-1916

US-09-107-133-1916

US-09-107-133-1916

US-09-107-133-1916
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-Q=/Cqq12_1/USPTD spoin_lh/US10724972/runat_03112005_141901_29159/app_query.fasta_1.519
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-UNTTY=Patents_NOUTFWT=Patents_NOUTFWT=Patents_NOUTFWT=Patents_NOT_0-NOUTFWT=Patents_NOT_0-NOUTFWT=Patents_NOT_0-NOUTFWT=Patents_NOT_0-NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=NOUTFWT=N
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Sequence 15, Appl
Sequence 15, Appl
Sequence 238, Appl
Sequence 238, Appl
Sequence 604, Appl
Sequence 604, Appl
Sequence 2556, Apl
Sequence 2556, Apl
Sequence 2556, Apl
Sequence 2556, Apl
Sequence 862, Appl
Sequence 862, Appl
                                                                                                     November 9, 2005, 12:50:22 ; Search time 214 Seconds (without alignments) 2561.461 Million cell updates/sec
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                                                                                                                                                                                                   GVESVRGLKILSVIGLLFVL.....EEMAKELVELSKKDSKKDNK 335
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                     nucleic search, using frame_plus_p2n model
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US-08-781-986A-355
US-09-830-217-15
US-10-278-946-15
US-08-956-171E-238
US-08-781-986A-238
US-08-781-986A-238
US-08-956-171E-2556
US-09-107-532A-862
US-09-134-001C-2655
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                                                                                                                                                                                                                                                                                                                                  1202784 seqs, 818138359 residues
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Maximum Match 100%
Listing first 45 summaries
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, Ygapext
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1690
1 GVESVRGLKILSVIGLIF
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Maximum DB seq length: 200000000
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Xgapop 10.0 ,
Ygapop 10.0 ,
Fgapop 6.0 ,
Delop 6.0 ,
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224.0
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Perfect score:
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9 Sequence 355, Application US/08781986A

Patent No. 6737248

GENERAL INFORMATION:
Patent No. 6737248

GENERAL INFORMATION:
STATIC OF INTERTION: Staphylococcus aureus Polynucleotides and Sequences
TITLE OF INTERTION: Staphylococcus aureus Polynucleotides and Sequences
TITLE OF INTERTION: Staphylococcus aureus Polynucleotides and Sequences
TITLE OF INTERTION: 5255
CORRESPONDENCES:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA

ZIP: 20850

COMPUTER: HP Vectra 486/33

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ArgGlyLeulleSerSerGluGluMetAlaLyBGluLeuValGluLeuSerLyBLyBABD 329
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                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 355:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                 TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 355:
                                                                                                  LENGTH: 668 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                          1.76e-45
475.00
86.89%
74.59%
28.11%
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Best Local Similarity:
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250 GlnMetAsnThrGluThrLeuSerGlnValAsnProGluArgMetPheileMetThrAsn 269
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Sequence 15, Application US/09830217

Sequence 15, Application US/09830217

GENERAL INFORMATION:
TITLE OF INVENTION: Staphylococcus aureus Genes and Polypeptides

FILE REFERENCE: PB461PCT
CURRENT APPLICATION UNMBER: US/09/830,217

CURRENT PILING DATE: 2001-04-24

PRIOR FILING DATE: 1999-03-18

PRIOR FILING DATE: 1999-03-18

PRIOR FILING DATE: 1998-04-01
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Matches:
Conservative:
Mismatches:
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      PILING DATE:
CLASSIFICATION: 435
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAK: (301) 309-8812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
US/08/781,986A
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475.00
86.89%
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APPLICATION NUMBER:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                  148 LysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThrIleSerLysAla 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuGlyLysGluGluGluGluGlyLysLysBrgLeuGluGluHisAspLysLysIleGluGlu 187
                                                                                                                                                                                             19 ATTAAAATGCTT---GTTGTTACGCTTGCTTTCCTACTTGTT---TTAGCAGATGTAGT 72
                                                                                                                                                                                                                      28 AsnAsnSerSerSerAsnSerSerLysGluSerSerLysAspGlyValGluIleLysHis 47
                                                                                                                                                                                                                                                                                             188 TyrLyslysGluIleThrMetAspLysAsnGlnLysValLeuProAlaValAlaAlaLys 207
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|TTCCAAAAA------GATGCAAAGCAAAGTATAAAGATGCATGGCATTGAAA 588
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Matches:
Conservative:
Mismatches:
Indels:
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PRIOR APPLICATION NUMBER: 60/084,674
PRIOR FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
LENGTH: 999
                                                               , ORGANISM: Staphylococcus aureus US-09-830-217-15
                                                                                                  7.57e-37
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Best Local Similarity:
Query Match:
DB:
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                                                        TYPE: DNA
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Leu-------LysGluLeuGluLysAspProValTrpLysLysLeuAsnAla 292
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                                                                                                                                              312 LeulleSerSerGluGluMetAlaLysGluLeuValGluLeuSerLysLysAspSerLys 331
                                                                                                                                                                                                                     931 TATAAATCTTCATTAAAACTTATGACGATTTATATGAA------AAGTTAAATTGAG 984
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73 GGGAATTCAAATAAACAATCATCATAACAAAGATAAGGAAACAACTTCAATTAAACAT 132
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                                                                                                                                                                                                                                                                                                                                                                                                                               JAPLICANT: Simpson et al.

APPLICANT: Simpson et al.

TITLE OF INVENTION: Staphylococcus aureus Genes and Polypeptides
FILE REFERENCE: P846,1USD1
CURRENT APPLICATION NUMBER: US/10/278,946
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: US/9/6199
PRIOR APPLICATION NUMBER: US 60/078,682
PRIOR APPLICATION NUMBER: US 60/078,682
PRIOR APPLICATION NUMBER: US 60/078,682
PRIOR FILING DATE: 1999-03-18
PRIOR FILING DATE: 1998-04-01
PRIOR FILING DATE: 1998-04-01
PRIOR FILING DATE: 1998-04-01
PRIOR FILING DATE: 1998-04-01
PRIOR FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Version 3.1
SEQ ID NO 15
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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US-10-278-946-15
'Sequence 15, Application US/10278946
'Patent No. 6821754
'GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Staphylococcus aureus
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51.74%
32.85%
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985 AAACAATCAAAA 996
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Percent Similarity:
Best Local Similarity:
Query Match:
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US-10-278-946-15
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Alignment Scores:
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Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
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                                                                                                                                        148 LysGerPhcAspGlyAspTyrAsnGluAsnIleAspAlaPhcLysThrlleSerLysAla 167
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LysAsnArg1le1leLysProLeuArgAspLys1leGlyLysTyrThrSerValGlyThr 107
                                              108 ArgLysGlnbroAsnLeuGluGluIleSerLysLeuLysProAspLeuIleIleAlaAsp 127
                                                          128 AsnAsnArgHisLysGlyIleTyrLysAspLeuAsnLysileAlaProThrIleGluLeu 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTTAAAAACAACCAAGTATCTGATGATTTAGATGAAATCACTTGGAACTTAGCTGGCGGA
                                                                                                                                                              ---rchactgatacagttttcaaattcaaa---gatacaactaagttaatggggaaggt
                                                                                                                                                                                                    TyrLyslysGluIleThrMetAspLysAsnGlnLysValLeuProAlaValAlaAlaLys
                                                                                                                                                                                                                                                                                ----SerTyrValGly
                        253 CAAAAACCGAAATTCGAATACATAAAAATGATTTAAAAGATACTAAGATTGTAGGTCAA
                                                                                                        ADDRESSEE: Human Genome Sciences, Inc
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                    SerGlyLeuLeuAlaHisProSerAsn--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 238, Application US/08956171E Setent No. 6593114 GENERAL INFORMATION: APPLICANT: Charles Kunsch Applicant: Gil H. Choi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
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US-08-956-171E-238
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CITY: Rockville

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148 LysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThrIleSerLysAla 167
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COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE. Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION NUMBER: US/08/956,171E
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: «UNKnown»
PRIOR APPLICATION AUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
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113
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                        NAME: Mark J. Hyman
REGISTRATION NUNBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NO: 238
                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (240) 314-1224
TELEPAX: (301) 309-8439
INFORMATION FOR SEG ID NO. 238:
SEQUENCE CHARACTERISTICS:
LENGTH: 3775 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
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405.00
51.74%
32.85%
23.96%
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FELECOMMUNICATION INFORMATION
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---TCTACTGATACAGTTTTCAAATTCAAA---GATACAACTAAGTTAATGGGGAAAGCT 522
                       LeuGlyLygsCluGluGlyLygLygLygLeuGluGluHigAspLygLygIleGluGlu 187
                                    207
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                                                                                                                                                                                                                                                                                                              LeulleSerSerGluGluMetAlaLysGluLeuValGluLeuSerLysLysAspSerLys 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 238, Application US/08781986A
Patent No. 6737248
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
                                                                  TyrLysLysGlulleThrMetAspLysAsnGlnLysValLeuProAlaValAlaAlaLys
                                                                                 ::::::|||
583 TTCCAAAAA--------GATGCAAAGCAAAGTATAAAGATGCCATTGAAA
                                                                                                                              221 GlnPheLeuSerGlnLeuGlyPheLysGluAlaLeuSerAspAspValThrLysGlyLeu
                                                                                                                                                                                    -----AATAAGACTTA
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                                                                                                                                                                        ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                              208 SerGlyLeuLeuAlaHisProSerAsn-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
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|1027 AAACAATCAAAA 1038
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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61 ATTAAAATGCTT---GTTGTTACGCTTGCTTTCCTACTTGTT---TTAGCAGGATGTAGT 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              235 GCCACTGACGTCGCTGTATCTTTAGGTGTTAAACCTGTAGGTGCTGTAGAATCATGGACA 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88 LysAsnArgllelleLysProLeuArgAspLysIleGlyLysTyrThrSerValGlyThr 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :::
295 CAAAAACGAAATTCGAATACATAAAAATGATTTAAAAGATACTAAGATTGTAGGTCAA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128 AsnAsnArgHisLysGlyIleTyrLysAspLeuAsnLysIleAlaProThrIleGluLeu 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148 LysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThrIleSerLysAla 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeuGlytysgluglugluglyLysLysArgLeuGluGluHisAspLysLysIleGluGlu 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188 TyrLysiyşGluIleThrMetAspLysAsnGlnLysValLeuProAlaValAlaAlaLys 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            221 GlnPheLeuSerGlnLeuGlyPheLysGluAlaLeuSerAspAspValThrLysGlyLeu 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48 GluGluGlyThrThrLysValProLysHisProLysArgValValValLeuGluTyrSer 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PheValAspAlaLeuValAlaLeuAspValLysProValGlyIleAlaAspAspAsnLys 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28 AsnAsnSerSerAsnSerSerLysGluSerSerLysAspGlyValGluIleLysHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208 SerGlyLeuLeuAlaHisProSerAsn---------SerTyrValGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       583 TTCCAAAAA-----GATGCAAAAGCAAAGTATAAAGATGCATGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   631 GCTTCAGTTGTTAACTTCCGTGCTGATCATACAAGAATTTATGCTGGTGGATATGCTGGT
                                                                                                                                                                                                                        3775
113
65
132
34
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                                                                                                                                                                                                                                           Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ength:
TELEPHONE: (301) 309-8504
INFORMATION FOR SEQ ID NO: 238:
SEQUENCE CHARACTERISTICS:
LENGTH: 3775 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                  5.58e-36
405.00
51.74%
32.85%
23.96%
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Best Local Similarity:
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292 AlavaliysAsnGlnArgValAspIleLeuAspArgAspLeuTrpAlaArgSerArgGly 311
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TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
TITLE OF INVENTION: Staphylococcus
TUTNE OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             254 GluThrLeuSerGlnValAgnProGluArgMetPhelleMetThrAsn----LysAlaSer 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      273 SerAsnGluProSerLeuLysGluLeuGluLysAspPro---ValTrpLysLysLeuAsn 291
                                                                                                                                                                                                                                                                                                                  123 CAGAGTACGTTAAAATCTGCATTTGCATTCGGTATCTCAAGAGCAGGTATGTTTATTAAT 182
                                                                                                                                                                                                                                                                                                                                                                               183 AATGAAGATACATTTATGGGACAATTCTTAATTAAAATGGGTATTCAACCTGAAGTCAAA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                  234 AspAspValThrLysGlyLeuSerLysTyrLeuLysGlyProTyrLeuGlnMetAsnThr 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                        194 MetAspLysAsnGlnLysValLeuProAlaValAlaAlaLysSerGlyLeuLeuAlaHis 213
                                                                                                                             154 TyrAsnGluAsnIleAspAlaPheLysThrIleSerLysAlaLeuGlyLysGluGluGlu 173
                                                                                                                                                                                                        174 GlyLysLysArgLeuGluGluHisAspLysLysIleGluGluTyrLysLysGluIleThr
                                                                                                                                                                                                                                                                                                                                                          214 ProSerAsnSerTyrValGlyGlnPheLeuSerGlnLeuGlyPheLysGluAlaLeuSer
                                                                                                                                                   312 LeulleSerSerGluGluMetAlaLysGluLeuValGluLeuSerLysLys 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-724-972A-6352 (1-335) x US-08-956-171E-604 (1-2115)
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Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb
COMPUTER: HP Vectra 486/33
OPBRATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US/08/781,986A
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US-08-781-986A-604
i Sequence 604, Application US/08781986A
j Patent No. 6737248
i GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: BENSON, BOD
REGISTRATION NUMBER: 30,446
 63.84%
37.85%
19.76%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: ASCII TEX
CURRENT APPLICATION DA
APPLICATION NUMBER:
     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20850
                                             Query Match
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Steam Street: 9410 Key West Avenue Street: 9410 Key West Avenue
                                                                                                                                                                                                                                                               913 GITAAAAACAACCAAGTATCTGATGATTTAGATGAAATCACTTGGAACTTAGCTGGCGGA 972
                                                                                                                                                                                                                                      312 LeulleSerSerGluGluMetAlaLysGluLeuValGluLeuSerLysLysAspSerLys 331
                                                                                                        293 yaliyaanginargyal---AsplieleuaspargaspleuTrpalaargserargGly 311
         GlnValAsnProGluArgMetPheIleMetThrAsnLysAlaSerSerAsnGluProSer 277
                                                                                    -----LysGluLeuGluLysAspProvalTrpLysLysLeuAsnAla 292
                                 COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskerte, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCIT Text

CURRENT APPLICATION DATE:

APPLICATION NUMBER: US/08/956,171E

FILING DATE: 20-Oct-1997

CLASSIPICATION: «Unknown>
PRIOR APPLICATION: «Unknown>
PRIOR APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:
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Matches:
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REGISTRATION UNDBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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US-08-956-171E-604
) Sequence 604, Application US/08956171E
) Retent No. 6593114
) GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 604:
SEQUENCE CHARACTERISTICS:
LENGTH: 2115 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                            1027 AAACAATCAAAA 1038
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Pred. No.:
Score:
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ELT. 7650-87/6-47/-01-8

PB248PP

Query Match: DB:

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Pred. No.:

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90.00%
82.50%
19.70%
                    9410 Key
                                CITY: Rockville
STATE: Maryland
COUNTRY: USA
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Best Local Similarity:
Query Match:
DB:
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Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                       154 TyrAsnGluAsnIleAspAlaPheLysThrIleSerLysAlaLeuGlyLysGluGluGlu 173
                                                                                                                                                                                                                                                                                                                                                                                                                                       174 GlyLyBLyBArgLeuGluGluHisAspLyBLyBLJeGluGluTyrLyBLyBLyBlulleThr 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                          194 MetAsplysAsnGlnLysValLeuProAlaValAlaAlaLysSerGlyLeuLeuAlaHis 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214 ProSerAsnSerTyrValGlyGlnPheLeuSerGlnLeuGlyPheLysGluAlaLeuSer 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183 AATGAAGATACATTTATGGGACAATTCTTAATTAAAATGGGTATTCAACCTGAAGTCAMA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234 AspAspValThrLysGlyLeuSerLysTyrLeuLysGlyProTyrLeuGlnMetAsnThr 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     254 GluThrLeuSerGlnValAsnProGluArgMetPheIleMetThrAsn---LysAlaSer 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||| |||:: :::||||||::
303 GAAGAACTTGCCAATATGAAAAGTTATGATTTTAGCCACTGACGGAAAACGGAC 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   470
                                                                                                                                                                                                                                                                                                                                                                                          273 SerAsnGluProSerLeuLysGluLeuGluLysAspPro---ValTrpLysLeuAsn 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         363 AAAAATAGAAGGAAATTC------ATTGATCCTGCAGTTTGGAAATCATTAAAA 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              292 AlavaliysAsnGlnArgvalAspIleLeuAspArgAspLeuTrpAlaArgSerArgGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeulleSerSerGluGluMetAlaLysGluLeuValGluLeuSerLysLys 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-724-972A-6352 (1-335) x US-08-781-986A-604 (1-2115)
                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                           Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2556, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Cil H. Choi
Patrick S. Dillon
REFERENCE/DOCKET NUMBER: PB246
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 604:
SEQUENCE CHARACTERISTICS:
LENGTH: 2115 base pairs
TYPE: nucleic acid
crabannennec. Acid
                                                                                                                                                                                                                     3.35e-28
334.00
63.84%
37.85%
                                                                                                                                         double
                                                                                                               TYPE: nucleac STRANDEDNESS: doub TOPOLOGY: linear
                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
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US-08-781-986A-604
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US-08-956-171E-2556
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ArgileileLysProLeuArgAspLysileGlyLysTyrThrSerValGlyThrArgLys 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 GlnProAsnieuGluGluIleSerLysLeuLysProAspLeuIleIleAlaAspAsnAsn 129
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US-08-701-966A-2556
WS-08-701-966A-2556, Application US/08781986A
Sequence 2556, Application US/08781986B
Sequence 2556, Application US/0878198B
Sequence 2556, Application US/0878198B
Sequence 2556, Application US/0878198B
Sequence 2556, Application US/087819B
Sequence 2556, Application US/08781B
Sequence 2556, Application US/0878B
Sequence 2556, Application US/
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
SOFTWARE: ASCII Text
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: MARK J. Hyman
REGISTRATION NUMBER: 46,789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 242 base pairs
TYPE: nucleic acid
TYRE: nucleic acid
TYRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2556:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PB248P1 TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (240) 314-1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 2556:
SEQUENCE CHARACTERISTICS:
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NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...1059
SEQUENCE DESCRIPTION: SEQ ID NO: 862:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5077
TELEPAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 862:
SEQUENCE CHARACTERISTICS:
LENGTH: 1059 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                       SOFTWARE: ASCII
CURRENT APPLICATION DATA:
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307.50
50.29$
31.29$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO
ORIGINAL SOURCE:
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Best Local Similarity:
Query Match:
DB:
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Sequence 862, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: BUTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 ArgHisLysGlylleTyrLysAspLeuAsnLysIleAlaProThrIleGluLeuLysSer 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90 ArgileileivsProbeuArgAsplysileGlyLysTyrThrSerValGlyThrArgLys 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110 GlnProAsnLeuGluGluIleSerLysLeuLysProAspLeuIleIleAlaAspAsnAsn 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 CGTATCATTAAACCAGTTAGAGAAAAATTGGGGATTATACTTCTGTAGGTACACGTAAA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 AspalaieuvalalaieudspvaliysProvalGlyileAlaAspaspAsniysiysAsn 89
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                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MADOS version 6.2

SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFTCATION ATA:
APPLICATION NUMBER: BAPLICATION NUMBER: BAPLICATION NUMBER: ATORNEY APPLICATION NUMBER: ATORNEY AGENT INFORMATION:
REFERENCY AGENT INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 2556:
SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-724-972A-6352 (1-335) x US-08-781-986A-2556 (1-242)
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Matches:
Conservative:
Mismatches:
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CITY: Waltham
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COMPUTER READABLE FORM:
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90.00%
82.50%
19.70%
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TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity:
Query Match:
DB:
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US-09-107-532A-862
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Pred. No.:
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118 GTAGTAGGTATCTTGATTCTAGCATTAGTTTA------GCA 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        337 GATAAGGTAGTTGGAGCAGCTACAAGCAGC-------CTTCCTGAGTATCTT 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 LysargvalvalvalteuGluTyrSerPheValaspAlaLeuValalaLeuAspVal--- 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 AlaCysGly-----AsnAsnSerSerSerAsnSerSerLysGluSerSer----- 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LysAspGlyValGluileLysHisGluGluGly---ThrThrLysValProLysHisPro
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Matches:
Conservative:
Mismatches:
Indels:
CURKENI AFELCATION DATA:

PRIOR PAPELCATION NUMBER: US/09/107,532A

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598

FILING DATE: 14 May 1998

FILING DATE: 14 May 1998

APTORNEY/AGENT: UNPORMATION:
NAME: AAIINIGHIO, PAMEN : 40,489

REFERENCE/DOCKET NUMBER: 40,489
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228

541

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RESULT 14

US-09-110-279-4042

is Sequence 4042, Application US/09710279

j Sequence 4042, Application US/09710279

j GENERAL INFORMATION:
j APPLICANT; KIMBRILY, WILLIAM JOHN

TITLE OF INVENTION: STAPHYLOCCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS

PILE REFERENCE: PU3480US

CURRENT APPLICATION NUMBER: US/09/710,279

CURRENT APPLICATION NUMBER: 06/164,258

PRIOR FILING DATE: 1999-11-09

NUMBER OF SEQ ID NOS: 4472

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 4042

LENGTH: 3267
                                                                                                                                                                                                                                                                                                                                                                                                                        LysGluAlaLeuSerAspAspValThrLysGlyLeuSerLysTyrLeuLysGlyProTyr 248
                                                                                                                                                                                                                                                                                                 249 LeuGln----MetAsnThrGluThrLeuSerGlnValAsnPro----------- 261
                                                                                                                                                                                                                                                                                                                  262 GluargMetPheIleMetThrAsnLysAlaSerSerAsnGluProSerLeuLysGluLeu 281
                                                                                                                                                                                                                                                                                                                                                                   282 GlulysAspProvalTrplysLysLeuAsnAlavalLysAsnGlnArgValAspIleLeu 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AspArgAspLeuTrpAlaArgSerArgGlyLeulleSerSerGluGluMetAlaLysGlu 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LysGlulleThrMetAspLysAsnGlnLysValLeuProAlaValAlaAlaLysSerGly 209
                                                                                                                                                            LeuLeuAlaHis---ProSerAsnSerTyrValGlyGlnPheLeuSerGlnLeuGlyPhe
                                                                                                                                                                                                             AsnGluAsnIle-----AspAlaPheLys------ThrIleSerLysAlaLeuGly
                                                             777 GATGACAACTTAATTAAAGATATGAAAAAAAATACAGAAAATTTAGGGAAAATCTACGAT
                                                                                        LysGluGluGluGlYLysLysArgLeuGluGluHisAspLysLysLyslieGluGluTyrLys
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104
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131
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
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296.50
47.54%
28.42%
17.54%
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CTHER INFORMATION:
US-09-710-279-4042
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Best Local Similarity:
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Pred. No.:
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|179 AAAGAAACTGTAACCATCAAAAATAGTTTTGAAGCAAGTGGTAAAGAAAATAATGGCAGT 1120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IleSerLysLeuLysProAspLeuIle---IleAlaAspAsnAsnArgHisLysGlyIle 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135 TyrLysAspLeuAsnLysIleAlaProThrIleGluLeuLysSerPheAspGlyAspTyr 154
     83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63
                                                                                                                  Sequence 3348, Application US/09710279
| Sequence 348, Application US/09710279
| Patent No. 6703492
| GENERAL INFORMATION:
| APPLICANT: KIMMERLY, WILLIAM JOHN
| TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
| TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
| CURRENT FILING DATE: 1034000.11-09
| PRIOR PILING DATE: 1999-11-09
| NUMBER OF SEQ ID NOS: 4472
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NO 3348
| LENGTH: 3153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LeuGluTyrSerPheValAspAlaLeuValAlaLeuAspValLysProValGlylleAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description of Artificial Sequence: synthetic nucleic acid sequence
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104
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                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                               ::: ||||||::::::
1015 ATTGATGAATTAAATGAA 1032
                                               LeuValGluLeuSerLys 327
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296.50
47.54%
28.42%
17.54%
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                -09-710-279-3348/c
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US-09-710-279-3348
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Db	RESULT 15 US-09-710-279-3564 ; Sequence 3564, Application US/09710279 ; Patent No. 670349ATION: ; APPLICANT: KIMMERLY, WILLIAM JOHN ; TITLE OF INVENTION: STARHYLOCCCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS ; FILE DEPENDENCE.	CURRENT APPLICATION NUMBER: US/09/710,279 CURRENT FILING DATE: 2000-11-09 PRIOR APPLICATION NUMBER: 60/164,258 NUMBER OF SEQ ID NOS: 4472 SOFTWARE: BAFFIT UST 2 1	SEQ ID NO 3564 LENGTH: 3618 TYPE: DNA ORGANISM: Artificial Se FEATURE: Artificial Se OTHER INFORMATION: Desc	Scores: 1.52e-23 296.50 milarity: 47.54%	Dest Docal Similarity: 28.42% Magmatches: Query Match: 17.54% Indels: DB: 4 Gaps: US-10-724-972A-6352 (1-335) x US-09-710-279-3664 (1-36	Qy 1 GlyValGluSerValArgGlyLeuLysIleLeuSerV	Oy 21 IlealaThralaalaCysGlyAsnAsnSerSerSerSerSerLysGluSerSer 39	QY 40 LygabpglyValgluIleLygHigglu	Qy 49GluGlyThrThrLygValProLygHisProLygArgValValVal 63	Qy 64 LeuGluTyrSerPheValAspAlaLeuValAlaLeuAspValLysProValGly11eAla 83	Qy 84 AspAspAsnLysLysAshArg11e11eLysProLeuArgAsp 97		Qy 116 IleSerLysLeuLysProAspLeuIleIleAlaAspAsnArgHisLysGlyIle	TyrlysAspleuAsnlys1leAlaProThr1leGluLeuLysSerPheAspGlyAspTyr
US-10-724-972A-6352 (1-335) x US-09-710-279-4042 (1-3267) OY 1 GlyValGluSerValArgGlyLeuLy8IleLeuSerValIleGlyLeuLeuPheValLeu 20		lval TGTA		98LV811eG1yLy8fyrThrSerValG1yThrArglysG1nProAsnLeuG1uG1u 115	15	155 AsnGluAsnIleAspAlaPheLysThrIleSerLysAlaLeuGly 169 	170 LysGluGluGlyLysLysArgLeuGluGluHisAspLysLysIleGluGluTyrLys 189	190 LysglulleThrMetAspLysAsnGlnLysValLeuProAlaValAlaAlaLysSerGly 209 ::: :: :: 1331 GATAAAACTAAAGACTTTAATAAGAAAGTAATGTATTTATTGGTTAACGAAGGTGAA 1387	210 LeuleualaHisProSerAsnSerTyrvalGlyGlnPheLeuSerGlnLeuGlyPhe 228 	229 LysGlualaLeuSerAspAspValThrLysGlyLeuSerLysTyrLeuLysGlyProTyr 248	249 LeuGinMetabnThrGluThrLeuSerGinValabnPro	262 GluArgMetPhelleMetThrAenLysAlaSerSerAenGluProSerLeuLysGluLeu 281 :::	282 GluLysAspProvalTrpLysLeuAsnAlavalLysAsnGlnArgValAspIleLeu 301 ::-	302 AspArgAspLeuTrpAlaArgSerArgGlyLeulleSerSerGluGluMetAlaLysGlu 321

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                                                                                                                                                                                                                                                                       LeullelleAlaAspAsnAsnArgHisLysGlyIleTyrLysAspLeuAsnLysIleAla
                                 AsnSerSerSerAsnSerSerLysGluSerSerLysAspGlyValGluIleLysHisGlu
                                                                                               GluGlyThrThrLysValProLysHisProLysArgValValValLeuGluTyrSerPhe
                                                                                                                               ValAspAlaLeuValAlaLeuAspValLysProValGlyIleAlaAspAspAspLysLys
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Patent No. 6703492
GENERAL INFORMATION:
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMID
FILE REFERENCE: PUJ480US
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 2000-11-09
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US-09-710-279-461
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Sequence 2690, Application US/09543681A

GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABII
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT PILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
                                                                                                                                                                                             CTATCAACGTTTGGACCAGGAAGATTTGGTGGTTTAGTGTTTGATACATTAGGATTT 1313
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      TIAGATGAATITIAAAAAAGCTGCACCAAAAGCTAAAGTT---GTATATGTAGGTACAAGT 1076
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Gatgacaacttaattaaagatatgaaaaaaatacagaaaattagggaaaatctacgat 1136
                                                                                         AspargaspieurrpalaargserargglyLeulleserserGluGlumetalaiysGlu 321
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Matches:
Conservative:
Mismatches:
Indels:
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85 TCGAAAAAGAAAAATAGTGATTCTAAAGAAACTGTAACCATCAAAAATAGTTTTGAAGCA 144
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                                                                             ; TYPE: DNA
; ORGANISM: Artificial Sequence
; FRATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-09-710-279-461
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101
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                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4412
SOFTHARE: Patentin Ver. 2.1
SEQ ID NO 461
LENGTH: 1044
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292.00
47.74%
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Best Local Similarity:
Query Match:
DB:
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ò		260 AsnProGluArgMetPhelleMetThrAsnLysAlaSerSer	AlaSerSer 273
q _Q		820 AATCCAGATGTTATTTTAGCTATGGATCGTGGTTCAGTTGTAGGTGGTGAAAGCAACAACA	:::::: GCAACAACA 879
. v		274 AgnGluProSerLeuLygGluLeuGluLygAspProValTrpLygLygLeuAsnAlaVal	29
}		LVBABDGlnArgValas	92
. 원 		925 AAAGTAATCATATTACGAATTAGATCAAAACTATGGTATTCTCTTCAGGA	GIVLeuile 313 GA 978
& a		314 SerSerGluGluMetAlaLygGluLeuValGluLeuSerLyg 327 979 TCTTCAACGACAACAAATTGATGAATGAA 1020	
RE:	RESULT 18 US-09-710-2' ; Sequence 3	.8 10-279-1267 ice 1267, Application US/09710279	
	Patent No GENERAL II APPLICAN	LIAM JOHN	
	TITLE OF FILE REFI	F INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS FERENCE: PU3480US APPLICATION NIMBED: 112/00/710, 270	AND PROTEINS
	CURRENT PRIOR API	FILING DATE: 2000-11-09 PPLICATION NUMBER: 60/164, 258	
•• •• •	NUMBER OF	: Filling DATE: 1999-11-09 FOR SEQ ID NOS: 4472 REF: Detail To 7 1	
	SEQ ID NO	1267 1044	
•• ••	TYPE: DN ORGANISM	TYPE: DNA DORONISM: Artificial Sequence	
-SD	OTHER IN OTHER IN	i FAILNES OTHER INFORMATION: Description of Artificial Sequence: synthetic ; OTHER INFORMATION: nucleic acid sequence US-09-710-279-1267	iic
Ali	gnment Sc		
Pre SCC Per Den DB:	Pred. No.: Score: Percent Simi Best Local S Query Match: DB:	Pred. No:: 7.74e-24 Length: 1044 Score: 292.00 Matches: 101 Percent Similarity: 47.74\$ Conservative: 68 Best Local Similarity: 28.53\$ Mismatches: 121 ' Ouery Match: 17.28\$ Indels: 64 DB:	
-sn	10-724-97	-1267 (1-104	
ò	т	16 LeuLeuPheValLeuIleAlaThrAlaAlaCysGlyAsnAsnSerSerSerAsnSerSer	snSerSer 35
Dp	2	25 TIATIGICICICIAGITITAGITITIAACGGCTIGIAGIAATAGITCGAATAATAGITCAACT	 ATTCAACT 84
ò	3	36 LysGluSerSerLysAspGlyValGlulleLysHisGlu-	48
q	60	::: B5 TCGAAAAAGAAAATGTGATTCTAAAGAAACTGTAACCATCAAAAATAGTTTTGAAGCA	TTGAAGCA 144
ò	4	49GluGlyThrThrLysValPro	ysvalPro 55
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ò	ß	56 LysHisProLysArgValValValLeuGluTyrSerPheValAspAlaLeuValAlaLeu	alAlaLeu 75
đ	20	205 AAGAATCCTAAAAATGCCGTTGTATTAGATTATGGAGCGCTTGATGTTGTTG	255
ò		76 AspValLysProvalGlyIleAlaAspAspAspAsnLys	LysAsn 89

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Genuence 2208, Application US/09902540

j Sequence 2208, Application US/09902540

j Patent No. 6833447

general information:
APPLICANT: Goldman, Barry S.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof TITLE OF INVENTION: WWBER: US/09/902,540

CURRENT APPLICATION NUMBER: 05/217,883

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

J EBNQTH: 702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 SeriyaTyrLeulyaGlyProTyrLeuGln---MetAsnThrGluThrLeuSerGlnVal 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProAlaValAlaAlaLysSerGlyLeuLeuAlaHis---ProSerAsnSerTyrValGly 220
                                                                                                    127 AspAsnAsnArgHisLysGlyIleTyrLysAspLeuAsnLysIleAlaProThrIleGlu 146
                                                                                                                                                                         ggaagaacagctaatcagaaaaatttagatgaatttaaaaaagctgcaccaaaagctaaa 489
                                                                                                                                                                                                      LeuLysSerPheAspGlyAspTyrAsnGluAsnIle-----AspAlaPheLys----- 162
                                                                                                                                                                                                                                                             ---ThrileSerLysAlaLeuGlyLysGluGluGluGlyLysLysArgLeuGluGluHis 181
                                                                                                                                                                                                                                                                              AsplyslysljeglugluTyrLyslysGlulleThrMetAsplysAshGlnLysValleu 201
                                                         CAATCTTTACCTAAATTTTTAGATGAATTTAAAGATGATAAGTATATTAATACTGGAAAT 369
-----AAAGAATTAGGTGTGGCTGATAAAGTAAAAGGTTTACCTAAAGGTGAAAATAAC 309
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                            90 ArgileileLysProLeuArgAsp-----LysileGlyLysTyrThrSerValGlyThr
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                                                                                     ArgiyeGlnProAsnLeuGluGluIleSerLysLeuLysProAspLeuIle---ileAla
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US-09-902-540-2208
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CGCGTAGCAGATTTAAAGAAAGCGCCTTGGAGATCAGTTAAAAACAAAAATCTCAGTTGTA 336
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                                                                                                                                                                                                                                                  ThrileGluLeuLysSerPheAspGlyAspTyrAsnGluAsnileAspAlaPheLysThr 163
                                                                                                                                                                                                                                                                                                                ACTGTATTCTCTGAGGAGCTGCGCGGAGATTGGAAATCAAAC------TTTAAGCTA 216
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                                                                                                                                                                                          143
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; Sequence 1583, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Gladen, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Miegand, Roger C.
; APPLICANT: Wiegand, Roger C.
; TILE OF INVENTION: Myxococus xanthus Genome Sequences and Uses Thereof F. FILE REPRENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
                                                                                                                                                                                                                                                                                                                                                              204 ValAlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPheLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeuLysGlyProTyrLeuGlnMetAsnThr-----GluThrLeuSerGlnValAsnPro
                                                                                                                                                                                                                                  IlelleAlaAspAsnAsnArgHisLysGlyIleTyrLysAspLeuAsnLysIleAlaPro
                                                                                                                                                                              104 ServalGlyThrArgLysGlnProAsnLeuGluGluIleSerLysLeuLysProAspLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          397 GATCAGCTTGGATTTGCTCGCCCTGAGTCTCAAGAC-----
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                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                  5.55e-24
291.00
51.95%
30.30%
; ORGANISM: Myxococcus xanthus US-09-902-540-2208
                                                                                               Best Local Similarity:
Query Match:
DB:
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US-09-902-540-1583
                                                                                  Percent Similarity:
                                           Alignment Scores:
Pred. No.:
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497 GATCAGCTATTTTACTTCTCTTATGAAACGGGAGACGGTGAAGCAAGAAGCTTGAAAAA 556
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Matches:
Conservative:
Mismatches:
Indels:
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; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1583
; LENGTH: 709
; TYPE: DNA
; ORGANISM: MYXCCCCUB XANTHUB
                                                                                                                           5.64e-24
291.00
51.95%
30.30%
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Best Local Similarity:
Query Match:
DB:
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US-09-071-035-37
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Sequence 37, Application US/09071035 Patent No. 6448043 GENERAL INFORMATION:

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APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     160 ACCAATGGTCAATTAACCGTTCCCAAAAATCCTAAGAAAGTCGTTGTTTTTGATAATGGT 219
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                                                                                                                                                                                                        COMPUTER TRADABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
FILING DATE:
CLASSIFICATION DATA:
PROOF APPLICATION DATA:
PRICATION WUMBER:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
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Matches:
Conservative:
Mismatches:
                                                                                 ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HANDEL A ANDERE BROOKES
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB369P2
FELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8510
TELEPHONE: (301) 309-8512
INPORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 975 base pairs
TYPE: nucleic acid
TYPE: 1000LOGY: linear
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283.00
48.19%
30.42%
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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Sequence 317, Application US/09134000C

| Requence 317, Application US/09134000C
| Patent No. 6617156
| GENERAL INFORMATION:
| APPLICANT: Lynn Doucette-Stamm et al APPLICANT: DOUCETC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: ENTERPOCCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS TITLE OF INVENTION NUMBER: US 60/055,778
| PRIOR APPLICATION NUMBER: US 60/055,778
| PRIOR FILING DATE: 1997-08-15
| NUMBER OF SEQ ID NOS: 6812
| SEQ ID NO 937
| LENGTH: 984
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                                                                                                                                                                                                                                                                                                                                                                        724 CATGGGCAAAGT-----------GTTTCTTACGAATATGTTTTA 756
                                                                                                                                                                                                                                                                                                                                                                                                      GlnValAsnProGluArgMetPhelleMet---ThrAsnLy8AlaSerSerAsnGluPro 276
                                                                                                                                                                                                                                                                                                                                                                                                                           GAAAAAAATCCTGGGATTCTCTTTGTGGTAGATCGCACCAAAGCAATTGGTGGCGACGAT 816
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                                                                                                                                                                                                                                                                               PheLeuSerGlnLeuGlyPheLysGluAlaLeuSerAspAsp------ValThr 237
                                                                                                                                                                                                                                                                                                  ProAlaValAlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGln 221
                                                                                       LysThrileSerLysAlaLeuGlyLysGluGluGluGlyLysLysArgLeuGluGluHis 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SerLeuLysGluLeuGluLysAspProValTrpLysLysLeuAsnAlaValLysAsnGln
ATT---TCTGGTCGTCAACAAGATTATCAAGAACAATTAAAAGCCATTGCGCCAACCATT
                              GluLeu------LysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPhe
                                                  ||||||||
| GGCACTATT-----TTTGATAAGAAGGAGGTAGCTAAAGAAAAAATAACTGGCTTA
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
Query Match:
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US-09-134-000C-937
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874 AAAGTCATTATGCTTCAACCAGATGTTTGGTATCTAAGCGGTGGTGGTGATTAGAATCAATG 933
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                                                                                                                                    AsnLysLysAsnArglleileLysProLeuArgAspLysIleGlyLysTyrThrSerVal 105
                                                                                                                                                                                                                              381
                                                      AAT-------ATCCCTGCGTATTTGAAAAATACCAAAAAGTTGAATCAGCA 321
                                        47
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                                                                                          317 GlumetAlaLysGluLeuValGluLeuSerLysLys 328
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Patent No. 6605709
GENERAL INFORMATION:
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Sequence 16, Application US/09891641

Sequence 16, Application US/09891641

GENERAL INFORMATION:
APPLICANT: Ve, Rick
APPLICANT: Wengy, Tao
TITLE OF INVENTION: NATURAL PROMOTERS FOR GENE EXPRESSION IN BACILLUS SPECIES
FILE REFERENCE: CL1686 US NA
CURRENT FILING DATE: 2001-06-26
NUMBER OF SEQ ID NOS: 81
SEQ ID NO 16
LENGTH: 954
                                                                251 MetAsnThrGluThrLeuSerGlnValAsnProGluArgMetPhelleMetThrAsnLys 270
                                                                                                                                    288
                                                                                                                                                                                       289 LysteuAsnAlaVallysAsnGlnArgValAspIleteuAspArgAspteuTrpAlaArg 308
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                                                                                     271 AlaSerSerAsnGluProSerLeuLysGlu-----LeuGluLysAspProValTrpLys
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802 GAAGCCATTGGTGCCGGTAAATTAGAGAAAAACACCTTTGAAAATGATGAAGTG---AAA
              LysGlyProTyrLeuGln
                                    LysileLeuSerVallleGlyLeuLeuPheValLeuIleAlaThrAlaAlaCysGlyAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 GluTyrSerPheValAspAlaLeuValAlaLeuAspValLysProValGly---IleAla
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Matches:
Conservative:
Mismatches:
Indels:
         LysGlyLeuSerLysTyrLeu
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276.50
48.62%
26.46%
16.36%
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; ORGANISM: Bacillus subtilis
US-09-891-641-16
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Best Local Similarity:
Query Match:
DB:
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      TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
CURRENT PRILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR PILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 1393
LENGTH: 978

LENGTH: 978

LENGTH: 978

CAGANISM: Proteus mirabilis
US-09-543-681A-1393
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94 AATACCTCAGTTACATACCAGCCTAATCAAATGTTGAAAACAGCAAAATGATAAAGTTGTT 153
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154 ATCAAGCACCTATTAGGTGAAACTGCAGTATCTAAAAATCCGTCTAAGGTTGTACTGTTT 213
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274 CCATTAGGAAATGCACCTGAATATTAAAGGGGCGTAITGCGAATGATGTG------
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TTAGCAACATTGAATACCGTGATTGAACAGGCTCAGAAAAA---GCGGCAGGATCAGAT
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
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GENERAL INFORMATION:
APPLICANT: G11 H. Choi
APPLICANT: G11 H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GluLeuGluLysAspprovalTrpLysLysLeuAsnAlaValLysAsnGlnArgValAsp 299
                                                                                                                                                                                                                                                                              ATCAGAATCAGACAAGGCAACATTTACATTTACCCTGAACAGGTGTATTTCAACTCCACA 645
                                                                                                                                                                                                                                                                                                                                                                       LysTyrLeuLysGlyProTyrLeuGlnMetAsnThrGluThrLeuSerGlnValAsnPro 261
                                                                                                                                                                                                                                                                                                                                                                                          GluArgMetPhelle---MetThrAsnLysAlaSerSerAsnGluPro---SerLeuLys 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                         grcaacrcagrodaccrcrcgcacaaggggggcacacricdaggaaagrccdrrrcrd 921
                                                                                                                                             CTTGCCCAGCTGACTGAAAAAAAAAAAAAAAAAATTATTGCAACTATGAACAG 525
                                                                                                                                                                                                       203 AlavalAlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPhe 222
                                                                                                                                                                                                                                                                                                           Leu --- SerGlnieuGlyPhelysGluAlaLeuSerAspAspValThrLysGlyLeuSer 241
                                                                                        ACGATCCCAGITICICATATCTCTTCAACTGGAAGGAAAACATG------ATGCTT 465
                                                                                                                        IleSerLysAlaLeuGlyLysGluGluGluGlyLysLysArgLeuGluGluHisAspLys 183
                                                                                                                                                                                  LysileGluGluTyrLysLysGluIleThr---MetAspLysAsnGlnLysValLeuPro 202
                                                           ThrileGluLeuLysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThr 163
                                                                                                                                                                                                                                                                                                                                          646 CTATACGGTGATTTTAGGCCTTAAG-----GCGCCGAACGAAGTAAAGGCTGCAAAAGCG
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ilelleAlaAspAsnAsnArgHisLysGlylleTyrLysAspLeuAsnLysIleAlaPro
                              Arcctrgctrcaacaaagttrccggaaaaaacgcrgcaaaaaatcagcacaggcacg
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COMPOTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
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Patent No. 6448043
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          253 ThrgluThrLeuSerGlnValAsnProGluArgMetPhelleMet---ThrAsnLysAla 271
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Mismatches:
Indels:
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Matches:
NAME: A. Anders Brookes

REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB369P2
RELEPROCE/DOCKET NUMBER: PB369P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
TELEFAX: (301) 309-8512
INFORMATION POR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 889 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-09-071-035-39
                                                                                                                                                                                                               3.47e-21
268.00
47.32%
30.28%
15.86%
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Best Local Similarity:
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Query Match:
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SerSerAsnGluProSerLeuLysGluLeuGluLysAspProValTrpLysLysLeuAsn 291
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PRIOR PRICK MILING DATE: 1999-0-28 (1993)444.3

PRIOR APPLICANTON WUMBRE: DE 1993122.1

PRIOR APPLICANTON WUMBRE: DE 1993122.1

PRIOR PLICANTON WUMBRE: DE 1993122.1

PRIOR PLICANTON WUMBRE: DE 1993122.1

PRIOR PLICANTON WUMBRE: DE 1993122.0

PRIOR PRICK APPLICATION WUMBRE: DE 1993122.0

PRIOR PLICANTON WUMBRE: DE 199312.0

PRIOR PLICANTON WUMB
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                                                                                                                                                                                                                                                                         312 LeulleSerSerGluGluMetAlaLysGluLeuValGluLeuSerLysLys 328
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191 GAAGCATCCACCAGCTCTGCGACTCGC-----GAATTCACAGACGCTCACGGAACAACC 244
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Matches:
Conservative:
Mismatches:
Indels:
PRIOR APPLICATION NUMBER: DE 19940764.9
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19940765.7
PRIOR APPLICATION NUMBER: DE 19940766.5
PRIOR FILING DATE: 1999-08-27
PRIOR FILING DATE: 1999-08-27
PRIOR PRIOR PRIOR DATE: 1999-08-27
PRIOR PRIOR PRIOR DATE: 1999-08-27
PRIOR PRIOR APPLICATION NUMBER: DE 19940831.9
PRIOR PRIOR DATE: 1999-08-27
PRIOR FILING DATE: 1999-08-27
PRIOR PRIOR DATE: 1999-08-31
PRIOR PRIOR DATE: 1999-03
PRIOR PRIOR DATE: 1999-03
PRIOR PLING DATE: 1999-03
PRIOR PLING DATE: 1999-03
PRIOR PLING DATE: 1999-03
PRIOR PLING DATE: 1999-09-03
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ORGANISM: Corynebacterium glutamicum
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266.00
44.79$
25.87$
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OTHER INFORMATION: RXN03084
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Best Local Similarity:
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23159 CTGTTCGAGCCTGACGAGGGCGCCGCGAAGCCGGAACCTCATCATCACC--- 23103
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                                              300 IleLeuaspargaspLeuTrpalaargSerArgGlyLeuIleSerSerGluGluMetala 319
                                                                        13 ATTTTAGACCGTGACTTATGGGCAAGATCACGTGGTTTAATTTCTTCAGAAGAATGGGCA 132
                72
                                                                                                                                                                                                                                                                          APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Wisgand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
FILE REPERIOR DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1250
LENGTH: 28194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 PheValAspAlaLeuValAlaLeuAspValLySProValGlyIleAlaAspAspAsnLyS
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3 CAGATTAGAAAAAGACCTGTATGGAAGAAATTAAACGCTGTGAAAAATCAACGTGTTGAT
                                                                                                              US-10-724-972A-6352 (1-335) x US-09-902-540-1250 (1-28194)
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                             Sequence 1250, Application US/09902540; Patent No. 6833447; GENERAL INFORMATION: APPLICANT: Goldman, Barry S. APPLICANT: Hinkle, Gregory J.
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257.00
50.16%
25.71%
15.21%
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Best Local Similarity:
Query Match:
DB:
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CURRENT APPLICATION NUMBER: US 60/064,964

PRIOR PILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-104

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

LENGTH: 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          286 ValTrpLysLysLeuAsnAlaValLysAsnGlnArgValAspIleLeuAspArgAspLeu 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           943
                                                                                                                                                                                                                                                                                                                                                                                                                   ---MetThrAsnLysAlaSerSerAsnGluProSerLeuLysGluLeuGluLysAspPro 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ThrMetAspLysAsnGlnLysValLeuProAlaValAlaAlaLysSerGlyLeuLeuAla 212
                                                                                                                                                                                                                                   650 GATGTCGAAGGTAAGACCGTCAACATGATTCGTCCCCGCGACGAGCAAACCATGAGCCTA 709
                                                                                                                                                                                                                                                                   HisproSerAsnSerTyrValGlyGlnPheleuSerGlnLeuGlyPheLysGluAlaLeu 232
                                                                                                                                                                                                                                                                                                                                  SerAspAspValThrLysGlyLeuSerLysTyrLeuLysGlyProTyrLeuGlnMetAsn 252
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                                                                                                                                        GluGlyLysLysArgLeuGluGluHisAspLysLysIleGluGluTyrLysLysGluIle 192
             GlyileTyrLysAspLeuAsnLysileAlaProThrileGluLeuLysSerPheAspGly 152
                                                                           153 AspTyrAsnGluasnIleAspAlaPheLysThrileSerLysAlaLeuGlyLysGluGlu 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ::: :::||||||||||||::: 539 CCGTGGBAGACAATGTC-----GTCTTCATCGGCGATGCATTGGGCAAGAGAG
                                                                                                                                                               306 TrpAlaArgSerArgGlyLeulleSerSerGluGluMetAlaLysGluLeu 322
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710 TACGGCCCGACCTCATTTGCCGGCAGCTCTTTGGAGTGCGCAGGA------
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Matches:
Conservative:
Mismatches:
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Gaps:
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265.00
96.43$
92.86$
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Best Local Similarity:
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US-09-134-001C-2023
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23042	22982	Gy 187 GluTyrLysLysLysLysLysAsnGlnLysValLeuProAlaValAlaAla 206 18.	226	GlyPheLysGluAlaLeuSerAspAspValThrLysGlyLeuSerLysTyrLeuLysGly	247	CGTC	22	Oy 285 ProvalTrpLysLysLeuAsnalavalLysAsnGlnArgValAsplleLeuAspArgAsp 304	305 LeuTrpAlaArgSerArgGlyLeuIleSerSerGluGluMetAlaLyeGluLeuVal 323	22589	RESULT 29 US-09-583-110-1062 ; Sequence 1062, Application US/09583110 ; Patent No. 6699703 ; GENERAL INFORMATION:	; APPLICANT: Lynn Doucette-Stamm et al.; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics ; FILE REFERRNCE: PATHON-079	; PRIOR APPLICATION NUMBER: US 60/085,131 ; PRIOR FILING DATE: 1998-05-12 ; PRIOR APPLICATION NUMBER: US 60/051,553 ; PRIOR FILING DATE: 1997-07-02	NUMBER OF SEQ ID NO SEQ ID NO 1062 LENGTH: 1035	ORGANISM: Streptococcus pneumoniae US-09-583-110-1062	Alignment Scores: Pred. No.: 254.00 Matches: 93 Score: Percent Similarity: 46.56\$ Best Local Similarity: 29.06\$ Mismatches: 119 Mismatches: 15.03\$ Indels: 14	.1062 (1-10	Oy 13 ValileGlyLeuLeuPheValLeuIleAlaThrAlaAlaCysGlyAsnAsnSer 30	glu

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4.6e-19
250.00
46.45%
27.22%
14.79%
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Best Local Similarity:
Query Match:
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8870 TCTGCTCCAACAAGTAACATTAAAAGTTCACTGGACGAGGTCAAACTTTCCAAAGTT 6811
                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 HislygGlylleTyrLygAspLeuAsnLysileAlaProThrileGluLeuLysSerPhe 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170 Lys-----GluGluGluGlyLysLysArgLeuGluGluHisAspLysLysJJeGluGlu 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------LeultgappLyslleGlyLysTyrThrServalGlyThrArgLysGln 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 ProLysArgValValValLeuGluTyrSerPheValAspAlaLeuValAlaLeuAspVal 77
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117
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COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                          ATTORNEY CART INPORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36.373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
INPORMATION FOR SEQ ID NO: 164: SEQUENCE CHARACTERISTICS:
LENGTH: 9707 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                6.67e-18
253.00
46.18
26.76
14.97
                                                                                              CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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Best Local Similarity:
Query Match:
DB:
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Sequence 312, Application US/09583110

Sequence 312, Application US/09583110

Parent No. 6699703

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al.

APPLICANT: Lynn Doucette-Stamm et al.

TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences

TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences

FILE REPERENCE: PATHOU-07A

CURRENT APPLICATION NUMBER: US 09/107,433

FRIOR PILING DATE: 1998-06-30

PRIOR FILING DATE: 1998-05-12

PRIOR FILING DATE: 1998-05-12

PRIOR APPLICATION NUMBER: US 60/051,553

PRIOR FILING DATE: 1998-05-12

SEQ ID NO 312

LENGHH: 966

LENGHH: 966

LENGHH: 966
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------CAAGAAGTCAGCTTTGAAAGTGTC 6238
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                                     |||||||
13.0 GICGCTACTAAAAATGAAAAAAGCCCTTGCGATCCTCCTTAATGAAGGA 6361
                                                                                                                                                                                                                                257 SerGlnValAsnProGluArgMetPhelleMetThrAsnLysAla------ 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                272 ---SerSerAsnGluProSerLeuLysGlu-----LeuGluLysAspProValTrpLys 288
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-----LysLysGlulleThrMetAspLysAsnGlnLys 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                309 SerArgGlyLeulleSerSerGluGluMetAlaLysGluLeuValGluLeuSerLysLyB
                                                                                                                                                                                           220 GlyGlnPheLeuSerGln---LeuGlyPheLys-----GluAlaLeuSerAspAspVal
                                                                                                                                                                                                                                                                                         237 ThrLysGlyLeuSerLysTyrLeuLysGlyProTyrLeuGlnMetAsnThrGluThrLeu
                                                                                                200 ValLeuProAlaValAlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrVal
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA; TYPE: DNA; ORGANISM: Streptococcus pneumoniae US-09-583-110-312
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION STREET: 100 Beaver Street CITY: Waltham STATE: Massachusetts COUNTRY: USA ZIP: 02354 COMPUTE: READABLE FORM: MEDIUM TYPE: CD/ROM IS09660 COMPUTE: <unknown> SOFTWARE: <unknown> COURRENT APPLICATION NUMBER: US/09/107,433</unknown></unknown>	FRIOR APPLICATION DATE: 30-Jun-1998 PRIOR APPLICATION DATE: 40/ 085131 PILING DATE: May 12, 1998 PILING DATE: May 12, 1998 PILING DATE: July 2, 1997 ATTORNEY/AGENT INFORMATION: REFERENCE/DOCKET UNMBER: 40/ 489 TELEPRENCE/DOCKET UNMBER: 40/ 489 TELEPROMUNICATION INFORMATION: TELEPROMUNICATION INFORMATION: TELEPROMUNICATION INFORMATION: TELEPROMUNICATION INFORMATION: TELEPROMUNICATION OF 98277	SEQUENCE CHARACTERISTICS: I LENGTH: 978 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: circular MOLECULE TYPE: DNA (genomic) HYPOTHETICE TYPE: DNA (genomic) ANTI-SENSE: NO ORIGINAL SOURCE: ORGANISM: Streptococcus pneumoniae FEATURE: NAMEKEY: misc_feature I LOCATION: (B) LOCATION 1978 SEQUENCE DESCRIPTION: SEO ID NO: 2206.	US-09-107-433-2206 Alignment Scores:	Qy 40 LysabpGlyValGluIleLysHisGluGluGlyThrThrLysValProLysHis 57 Db 121 TCTGCTCCAACAGGGTAACCATTAAAAGTTCACTGGACGTCAAACTTTCCAAAGTT 180 Qy 58 ProLysArgValValValLeuGluTyrSerPheValAspAlaLeuValAlaLeuAspVal 77 Db 181 CCTGAAAAGATTGTGACCTCGGCGCTGCGGATACTATTCGCGCTTTAGGATTT 240 Qy 78 LysProValGlyIleAlaAspAspAsnLysLysAsnArgIleIleLysPro
TAAAAGTTCACTGGACGAGGTCAAACTTTCCAAAGTT 168 IUTYrSerPheValAspalaLeuValAlaLeuAspVal 77 ::	LeulellealaAspasnAsnArg 130		yrLeuGlnMetAsnThrGluThrLeuSerGln 258 :::::::: :::::: ::: ::::::::::	1GluLeuSeriysiya 328 ::::::::
TCTGCTCCAACAGAGGTAACCAY ProbysArgValValValLeuG] CTGAAAAGATTGTGACCTTTG LysProValGlyIleAlaAspAe	111 ProAsnLeuGluGlulleSerLysLeuLysProAspLeullelleAlaAspAsnAsnAsnArg 322 C	499 GAAACTGGTACACAGAAGCCAAGGAAATTGGCCAAGCTAGACAAGGACATCCAAGAA 188 Tyr	239 GlyLeuSerLysTyrLeuLysGlyProTyrLeuGlnMetAsnThrGluThrLeuSerGln	Oy 311 GlyLeulleSerSerGluGluMethlaLysGluLeuValGluLeuSerLysLys 328 ::: ::::: :::::

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PRIOR APPLICATION NUMBER: DE 19932228.7
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR PILING DATE: 1999-07-09
PRIOR PPLICATION NUMBER: DE 19932230.9
PRIOR PPLICATION NUMBER: DE 19932230.9
PRIOR PPLICATION NUMBER: DE 19932230.9
PRIOR PPLICATION NUMBER: DE 1993297.3
PRIOR APPLICATION NUMBER: DE 19933006.9
PRIOR PLILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19933006.9
PRIOR PLILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19933006.9
PRIOR PLILING DATE: 1999-08-27
PRIOR PRILING DATE: 1999-08-31
PRIOR PLILING DATE: 1999-09-03
PRIOR PRILING DATE: 1999-09-03
PRIOR PLILING DATE: 1999-09-03
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APPLICATION NUMBER: DE 19932209.0
FILING DATE: 1999-07-09
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FILING DATE: 1999-07-09
APPLICATION NUMBER: DE 19932227.9
                                         FILING DATE: 1999-07-09
APPLICATION NUMBER: DE 19912125.6
FILING DATE: 1999-07-09
APPLICATION NUMBER: DE 19912128.0
FILING DATE: 1999-07-09
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APPLICATION NUMBER: DE 19932190.6
APPLICATION NUMBER: DE 19932191.4
APPLICATION NUMBER: DE 19932191.4
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                DE 19932124.8
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ORGANISM: Corynebacterium glutamicum
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US-09-602-787A-597
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APPLICANT: Sch"der, Hartwig
APPLICANT: Lalder, OBKAr
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORYNBBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OF INVENTION: TRANSPORT
TITLE OF INVENTION: TRANSPORT
FILE OF INVENTION: TRANSPORT
FILE OF INVENTION: TRANSPORT
FILE OF INVENTION: DIVOLVED IN MEMBRANE
CURRENT APPLICATION NUMBER: US/09/602,787A
CURRENT FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: DE 19931454.3
PRIOR APPLICATION NUMBER: DE 19931478.0
PRIOR APPLICATION NUMBER: DE 19931478.0
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931563.9
PRIOR PLING DATE: 1999-07-08
PRIOR PLING DATE: 1999-07-08
PRIOR PLING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 1993122.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         200 ValLeuProAjaValAlaAjaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrVal 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   220 GlyGlnPheLeuSerGln---LeuGlyPheLysGluAlaLeuSerAspAspValThrLys 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239 GlyLeuSerLysTyrLeuLysGlyProTyrLeuGlnMetAsnThrGluThrLeuSerGln 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 GAAGACTCACGCCACGGACAA------GAAGTCAGCTTTGAAAGTGTCAAAGAA 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---derigerakahargarrarceakerakacaceadacererakarerakadega 921
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571 GTCGCTACTAAAAATGAAAAAGGCCCTTGCGATCCTCCTTAATGAAGGA 630
                                                                                                                                                                                                                 151 AspGlyAspTyrAsnGluAsnIleAspAla---PheLysThrIleSerLysAlaLeuGly 169
                                                                                                                                                                                                                                                                                                                        170 Lys-----GluGluGluGlyLysLysArgLeuGluGluHisAspLysLysIleGluGlu 187
ProAsnLeuGluGluIleSerLysLeuLysProAspLeuIleIleAlaAspAsnAsnArg 130
                                                                                                       131 HistysGlylleTyrLysAspLeuAsnLysileAlaProThrileGluLeuLysSerPhe 150
                                                                                                                                     311 GlyLeuIleSerSerGluGluMetAlaLysGluLeuValGluLeuSerLysLys 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 631 AAAATGGCAGCCTTTGGTGCCAAATCTCGTTTC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pequence 597, Application US/09602787A
Patent No. 6696561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Pompejus, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-602-787A-597
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235 295 83 AlaAspAspAsnLysLysAsnArgIleIleLysProLeuArgAspLysIle-----Gly 100 356 ACCGGATACAAATTCTTCGAAAACGGATTGGGACCGTGGACTGATGAGTTAGTGGAAAGGC 415 101 Lys --- TyrThrSerValGlyThrArgLysGlnProAsnLeuGluGluIleSerLysLeu 119 120 LysprokspleuileileAlaAspAsnAsnArgHisLysGly---IleTyrLysAspleu 138 Lysileteu-----ServalileGlyLeuLeuPhevalLeulleAlaThrAlaAlaCys 26 139 АвпLувіleAlaProThrIleGluLeuLysSerPheAspGlyAspTyrAsn---GluAsn 157 ::: |||||||||| ::: 536 TCTGATATCGCACCGGTGGTCGCGGGGAACAGCTGCATACGCAGTAGCTCGC 595 158 IleAspAlaPheLysThrIleSerLysAlaLeuGlyLysGluGluGluGlyLysLysArg 177 LeuGluGluHisAspLysLysIleGluGluTyrLysLysGluIleThrMetAspLysAsn 197 656 AATGAGGAACAGATGCTCTGATCCAAGCTGCGCGT------GATGAAAAT 700 198 GlnLysValLeuProAlaValAlaAlaLysSerGlyLeuLeuAlaHisPro----- 214 42 62 63 ValLeuGluTyrSerPheValAgpAlaLeuValAlaLeuAspValLysProValGlyIle 82 27 GlyAsnAsnSer-----SerSerAsnSerSerLysGluSerSerLysAspGly 176 TCTAACAATGCAGATGACACCGACGCTGATTCAACATCCACGGAAACTCCGCTTTTCCT ValGlulleLy8HisGluGluGlyThrThrLy8ValProLy8HisProLysArgValVal US-10-724-972A-6352 (1-335) x US-09-602-787A-597 (1-1119) Score:
Percent Similar
Best Local Simi.
Query Match:
DB: 43 178 Pred. No.: е В ò 셤 a g ઠે ò ઠે ઠે g ò 유 ઠે g ò g ઠે 임 8 6 a ठे

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è 8	316		AlaLysGluLeuVal GCACCACGTATTGCT	GluGluMetAlaiysGluLeuValGluLeuSerLysLysBaspSer ::: GAACATCTCGCACCACGTATTGCTGAGGTTTGAAGTAAACTC	AspSer 330 ::: AACTCA 1105
RESULT US-09-15 Pate 15 Pate 1	ILT 34 guence 31 guence 31 fuent No. 31 fuence 31 interest No.	8, Applica 6562958 ORMATION: Gary D. B NVENTION: BNCE: GTC9: PLICATION: LING DATE: SEQ ID NOS 350 ID NOS 75	318 See Application US/09328335562958 RWATION: Gary L. Breton et al. VENTION: NUCLEIC ACID AN VENTION: BAUMANNII FOR I NUCE GTC99-018A FILGATION NUMBER: US/09/3 ING DATE: 1999-06-04 ESQ ID NOS: 8252 B Acinetobacter baumannii 318	RESULT 34 US-09-228-352-318 i Sequence 318, Application US/09328352 patent No. 6562958 i GENERAL INFORMATION: i TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS TITLE OF SEPERACE: GTC99-03PA CURRENT APPLICATION UNBER: US/09/328,352 CURRENT FILING DATE: 1999-06-04 i NUMBER OF SEQ ID NOS: 8252 i LENGTH: 975 j TYPE: DAA ORGANISM: Acinetobacter baumannii US-09-328-332-318	OUENCES RELATING TO ACINETOBACTER THERAPEUTICS
Alignm Pred. Score: Percen Best L Query	Alignment Scores Pred. No.: Score: Percent Similari Best Local Simil Query Match:	res: arity: nilarity:	5.05e-18 241.00 47.42\$ 24.01\$ 14.26\$	Length: Matches: Conservative: Mismatches: Indens: Gaps:	975 79 77 135 38 10
US-10-	-724-972A	-6352 (1-	335) x US-09-32	8-352-318 (1-97	5)
& 8	14	IleglyLeuI ::: GTCGCCCTCA	LeuPheValLeuIle ::: ATCATAGCGGCAGCT	AlaThrAlaAlaCys(GTCACTCTACAAGCAI	lledlyLeuLeuPheValLeuIleAlaThrAlaAlaCysGlyAsnAsnSerSerSerAsn 33 ::: ::: GTGGCCTCATCATAGGGGGAGCTGTCACTCTACAAGCATGTGAAAAGTTGAAGAT
ờ	34	SerSerLysG	SerSerLysGluSerSerLys	AspGlvValGluI	, u
qq		ACCACTCAAC	 	GCAGAACCGATTACGC	ACCACTCAAGCTTCTCAGAAGCTAGCAGAACGATTACGGTAAAACATGCGCTTGGAACT 153
'n	52	ThrLysValF	ProLysHisProLys	ArgvalvalvalLeuC	iluTyrSerPheValAspAla 71
qa	154	ACGGTGATAG	SATCATCTACCGCAA		
ð i		LeuValAlaI	.euAspValLysPro	ValGlyIleAlaAspA	LeuValAlaLeuAspValLysProValGlyIleAlaAspAspAsnLysLysAsnArglle 91
qa (4	CTAGATCAAC	ricaardricecearr.	ATGGGAATGCCAAAAG	ATTATGTTCCACACTTTTTG 273
දු පු	274	IleLysProLeuArgAsp AaaaaTaTaaaaagAT	.euArgAspLysIle ::: \AAAAAGAT(<pre>3lyLysTyrThrSerV ::: 3CACAAATTCAGGATT</pre>	IleLysProLeuArgAspLysIleGlyLysTyrThrSerValGlyThrArgLysGlnPro
ò	112	AsnLeuGluG	lulleSerLysLeul	LysProAspLeuilei	leAlaAspAsnAsnArgHis 131
Ωp	328	::: AATATGGAAA	 GGATATATGCATTA		:: AATATGGAAAGGATATATGCATTAAAACCAGACCTGATTTTGATGACGCCATTACAC 384
ò		LysGly1leT 	YrLysAspLeuAsnl	LysGlyIleTyrLysAspLeuAsnLysIleAlaProThrIleGluLeuLysS. ::::: :::	leGluLeuLysSerPheAsp 151
d d	385 (GTTAATCAGT	Arcaggaacigica	AAATTGCCCCGACCA	Trcarracgar 435
දු පු	152 (GlyaspTyrasnGluasn- ::::: ATTAACTTCAACAATAGCG	ISDG1uAsn 	ATCATATTGGTCTGG	GlyAepTyrAenGluAen
è		10001			,
6 6	194	ileserrysa ::: TTAGGAAAAA	eserrysarareuglyrysglud ::: TTAGGAAAATATTTAATAAAGAAG	SluGluGlyĽysĽysA ::: :ATTTAGCCCGCCAGA	11eestrybalaleuulykybuluuluulykybkyakapleuoluoluHisaaspiys 183 1.
ò		LysileGluG	luTyrLysLysGlul	leThrMetAspLysA	0

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Alignment Scores:
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Sequence 69, Application US/09071035

Parcent No. 644804010

GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Nockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                               276 ProserteulysGluteuGluLysAspProValTrpLysLysLeuAsnAlaValLysAsn 295
                                                                                                                                                                                                                                                           296 GlnargyalAspileLeuaspargaspLeuTrpalaargSerargGlyLeuIleSerSer 315
                                                                                                                                                                                                                                                                       224 SerGlnLeuGlyPheLysGluAla-----LeuSerAspAspValThrLysGlyLeuSer 241
                                                                                                                        LysTyrLeuLysGlyProTyrLeuGlnMetAsnThrGluThrLeuSerGlnValAsnPro 261
                                                                                                                                       CAAGTGAAGCAAGTA---CAAGCCGTAACGGCCAATGGCCCAGAAAGAGCATTAGTCGTT
                                  204 ValAlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPheLeu
                                                  :::
613 CTTCATAACAATGGGGCATTTAGTAATTTTGGTATTCAGTCACGCTATGGCTTTATTTTT
                                                                                            storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE:
MEDIUM TYPE:
Diskette, 3.50 inch, 1.4Mb stc
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOCTWARE: ASCII Text
CURBINT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
                                                                                                                                                                                                                                                                                                        316 GluGluMetAlaLysGluLeuValGlu 324
                                                                                                                                                                                                                                                                                                                     NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REPERENCE/DOCKET NUMBER: P8369P2
TELECOMMUNICATION INPORMATION:
TELEPHONE: (301) 309-8504
TELEPRAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 954 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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US-09-071-035-69
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US-09-071-035-69
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229 LysGluAlaLeuSerAspAspValThrLysGlyLeuSerLysTyrLeuLysGlyProTyr 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           269 AsnLysAlaSerSerAsnGluProSerLeuLysGluLeuGluLysAspProValTrpLys 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----LysiysileGluGjuTyr-----LysiysGluIleThrMetAspLysAsnGln 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LysvalLeuProAlaValAlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyr 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuArgAspLys1leGlyLysTyrThrSerValGlyThrArgLysGlnProAsnLeu--- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------GluGlulleSeriysLeuLysProAspLeullelleAlaAspAsn 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             313 TATGACTIGCCATAIGAAGCGGTICTAAAATITGAACCTGACTTATTATTAATCAGTICA 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Asnarg-----HislysGlylleTyrLysAspLeuAsnLysIleAlaProThrlleGlu 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeulysSerPhcAspGlyAspTyrAsnGluAsnIle-----AspAlaPhcLysThr 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTCAAAAAC-------GGCGAAAATGTCACCTGGCGTGATCAATTGGAAGAT 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IleSerLysAlaLeuGlyLysGluGluGluGlyLysLysArgLeuGluGluHisAsp--- 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -------GTCCCCACTATTTCC 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----CATGAAGTAACAGATACCTTAGGCAATAAAGTAACGTCCTCCCGCGAAACCCAAA 180
                                                                                                                                                                                                                                                                                                            Argvalvalval-----LeuGluTyrSerPhevalAspAlaLeuvalAlaLeuAspVal 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LysprovalGly-----IleAlaAspAspAsnLysLysAsnArglleIleLysPro 94
                                                                                                                                                            LeulyslleLeuSerVallleGly-----LeuLeuPheValLeulleAlaThrAlaAla 25
                                                                                                                                                                                                                                     26 ÇyşGİYAsın---AsınSerSerSerAsınSerSerLysGluSerSerLysAspGlyValGlu 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                679 CAA-----GITCCAAAATTAGTGGAAGAAATTTCTAAAAACGCTACTGCGGATTGG
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TTAAAAAAGACGGTCCTAATTGGTACAACCCTTCTTCTTTGGTTCATTCTTACTCGCAGCT
954
999
103
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94
                                                                                                                              (1-335) x US-09-071-035-69 (1-954)
 Length:
Matches:
Conservative:
Mismatches:
Indels:
6.36e-18
240.00
45.28%
27.50%
14.20%
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                                Percent Similarity:
Best Local Similarity:
Query Match:
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0y 204 ValAlaAlaLysSerGlyLeuLeuAlaHisProSerAmserTyrValGlyGlnPheleu 223 66 GTGCTCCCGGGGGGGCTATGGGCGCTTTGGGCGTTTGGGCGTTTGGGCTTTGGGTTGGGG 224 SerGlnLeuGlyPhelyGluhlaLeuSerApaPaylaThrLygGlyLeuSerLysTyr 243 256 GGTGATTGGGGGGGCGCTGGGGGGGTTG	PRIOR APPLICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: ATTORNEY AGENT: ATTORNEY AGENT: ATTORNEY Brookes, A. Anders REGISTRATION NUMBER: 36,373 REFERENCE/DOCKET NUMBER: 36,373 FELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504 TELEFAX: (301) 309-8512 INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS: LENGTH: 895 base pairs TOPOLOGY: linear TOPOLOGY: linear Alignment Scores: Red. No.: 1.66e-17 Length: 895 Score: 236.00 Matches: 88
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CTCATGATTGAAGACATACAAAAAGCTTTGAAA 895
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APPLICATION NUMBER: 08/961,083
PILING DATE: OCT-30-1997
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marker
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB340P3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 895 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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236.00
46.22%
26.59%
13.96%
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                             GlylystyrThrSerValGlyThrArgLysGlnProAsnLeuGluGluIleSerLysLeu 119
                                                                                                                                                                                                                                                                                                       LysproAspleuileileAlaAspAsnAsnArgHisLysGlyIleTyrLysAspLeuAsn 139
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         Conservative:
Mismatches:
Indels:
Gaps:
                                                              US-10-724-972A-6352 (1-335) x US-08-961-083-23 (1-895)
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            46.22%
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Best Local Similarity:
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GlyLysTyrThrSerValGlyThrArgLysGlnProAsnLeuGluGluIleSerLysLeu 119
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| GAAAAAATTGTCGGAATGCCTACAAAACTGTTCCGACTTATCTAAAAAAAGACCTAGTG 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 AGTTCACTGGACGACGTCAAACTTTCCAAAGTTCCTGAAAAAATGTGACCTTTGACCTC 127
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                                                                                                                                                                                       ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NOMBER: US/09/536,784
FILING DATE: 30-Oct-1997
CLASSIFICATION: CURNOWN>
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Conservative:
Mismatches:
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93 94 92 19

Matches: Conservative: Mismatches: Indels: Gaps:

Db 221 GGAACT	GTCAAAAATGTTGG	STTCTATGAAAGAA	GTCAAAAATGTTGGTTCTATGAAAGAACCTGATTTAGAAGCTATCGCCGTT	ATCGCCGCCCTT 280	_	3		;
Oy 120 LysPro ::: Db 281 GAGCCT	OASpLeulleileal 	aAspAsnAsnArgi TTCGCCACGTACA	AspleullellealaaspasnasnargHislysGlylleTyrLysaspleuasn	вргецАвп	1	Percent 8 Best Loca Query Mat	Percent Similarity: Best Local Similarity: Query Match:	236.00 45.61% 27.19% 13.96%
Oy 140 Lysile	AlaProThrileGl	uLeulyaSerDhez	eAlabrothrileGluLeulveSerbbaaeclivanmunicalina			DB:		4
Db 338 GAAATC	GCCCAACCGTTCT	CTTCCAAGCAAGC	GAAATCGCCCCAACCGTTCTTTCCAAGCAAGCAAGAATAACTGAAATAATTGAAAAAAAA	::: CTTCTACCAAC 267		US-10-724	-972A-6352 (1	-335) × US-
Oy 160 Ala	PheLysThrileSe	rLysAlaLeuGlyI	PhelysThr11eSerLysAlaLeuGlyLysGluGluGluGlyLysLys			පි සි	24 AlaAlaCysGlyAsnA 	8GlyAsnA
Db 398 GCTAAT	ATCGAATCCTTAGC	: : AAGTGCCTTCGGCC		AAGCCAAGGAA 457		ìò		WEH! AG ING
177 ArgLeu	GluGluHisAspLysLysIleGluGluTyr-	stysileGluGluT	yr	188		g Q		CATGAAG
458 GAATTG	ACCAAGCTAGACAA	GAGCATCCAAGAAG	accaagctagacaaggcatccaagaagtcgctactaaaaatgaaagctctgac	AAAGCTCTGAC 517		ò	58 ProLysArgv	rgValValVal-
LYSLYS	3luIleThrMetAsp	pLysAsnGlnLysV :::	GlulleThrMetAspLysAsnGlnLysValLeuProAlaValAlaAlaLysSer	laAlaLysser 208		qq	 127 CCCAAACGGA	
SIB AAAAAA	SCCTTGCGATCCT	CCTTAATGAAGGAA	GCCCTTGCGATCCTCCTTAATGAAGGAAAAATGGCAGCCTTTGGTGCCAAATCT	Greccadarer 577		ò	76 AspValLysProValGly	rovalGly-
209 GlyLeu	leuAlaHisProSeı	rAsnSerTyrValG	LeuAlaHisProSerAsnSerTyrValGlyGlnPheLeuSerGlnLeuGly	lnLeuGly 227	_	qq	175 GGAGAAAACCAGTGGCAC	 CAGTGGCAC
228			rettetaccaaacciigaaa			ò	93 LysProLeuA	SProteuArgAspLysI
608 TTCAAA	CCAACTCATACAAAAATTTCAACTCAACTCAACTCAAC	iserAspAspValT ::: http://www.asp.	GlualareuserAspasDvalThrLysGlyLeuSerLysTyrLeuLys			QQ	235 AAAGAATTGAAAGAT	AAGAT
246 Glvbro	Ver Out I make the	ATTTGAAGACTCAC	SCCACGGA	649		ò	113 Leu	
650	::::::::::::::::::::::::::::::::::::::	TINTGLUTATLEUS	17. LeugilmeckbninglüffleuserGinValAsnProGludrgMetPhe 1			qq	259 ATTECTATGACTTGCCAL	ACTIGCCAL
IleMet	Thrasnivsala		Sough and the second se			ò		rgH:
GTCATC	ACCGTACCCTTGCC	ATCGGTGGGACA	AACCGTACCCTTGCCATCGGTGGGGACAAATTTAGGTAAAATTTAAAAAAAA	COSETLEULYS 279		තු .		CTCTAGTTG
Oy 280 Glu	LeuGluLysAsp	ProValTrpLysLy	LeuGluLysAspProValTrpLysLysLeuAsnAlaValLy			કે દ	145 IleGluLeuLysSer	/sSerPheA
Db 761 AATGCCC	::: CTTATCGCTGAAACACCT	 CCT	 GCTGCTAA	 AAATGGTAAG		} }		
298 ValAspI	leLeuAspArgAsp	LeuTrpAlaArgSe	leLeuAspArgAspLeuTrpAlaArgSerArgGlyLeulleSerSerGluGlu		_	qq		SCACTGTTT
903 ATTATCO	aactaacacagac	CTCTGGTATCTAAC		::: ATCAACAAAA 862		ò		-LvstvsI
318 MetAlaI	ysGluLeuValGluLeuSerLysLys		328			Dp	— ც	CAAAGGCG
863 CTCATGA	ttgaagacatacaaaaagctttgaaa		895		_	δ	197 AsnGlnLysValLeuProAl	lLeuProAl
RESULT 39 US-09-134-000C-2609						Dp	529	
Sequence 2609, Appl. Patent No. 6617156	cation US/091	34000C			_	٥٨	217 SerTyrval	
APPLICANT: Lynn Dor	: ucette-Stamm et	t al				QQ	::: 565 AACCAAGICTTTAIGGITAG	TATGGTTAG
TILLE OF INVENTION: NUCLEIC ACID AND AMINO ACI	: NUCLEIC ACID	AND AMINO ACI S FAECALIS FOR	ACID SEQUENCES RELATING TO FOR DIAGNOSTICS AND THERAP	ATING TO D THERAPEUTICS		٥٨	227 GlyPheLysGluAlaLeuSe	uAlaLeuSe
CURRENT APPLICATION	N NUMBER: US/05	9/134,000C				q a	625 GGCCTCCAA	GT
PRIOR APPLICATION N	S: 1998-08-13 VUMBER: US 60/0	055,778				ò	247 ProTyrLeuGlnMetAsnTh	nMetAsnTh
NUMBER OF SEQ ID NO	1997-08-15 0S: 6812				ш	Db	676 GATTGGAATCAAGTTTCTTT	AGTTTCTTT
SEQ ID NO 2609	version 3.1					δ	267 MetThrAsnLysAlaSerSe	sAlaSerSe
	occura faecalia				-		736 GTAAACAGCGATGAATCAGC	TGAATCAGC
C-2609	3					č	287 TrpLysLysLeuAsnAlaVa	uAsnAlaVa
Alignment Scores: Pred. No.:	1 70-17	7	•			qa	778 IGGAAGAACTTACCTGCTGT	Accrecrer
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US-10-724	-972A-6352 (1-335) x US-	
ζō	24 AlaalaCysGlyAsnAsnSerSerSerAsnSerSerLysGluSerSerLysAspGly 42	
QQ	GCTTGTGGTAATACGAATAAAGAAGCCAACAACGCTGACAAAACA7	
δ	ValProLysHis 5	
οQ	4	10
ò	58 ProbysArgValValValLeuGluTyrSerPheValAspAlaLeuValAlaLeu 75	
Ор	127 CCCAAACGGATTATTGCGAGTTATTAGAAGATTATCTAGTTGCATTA 174	
ò	76 AspValLysProValGlyIleAlaAspAspAsnLysLysAsnArgllelle 92	
qq	175 GGAGAAAACCAGTGGCACAATGGACAGTTGACAAGGCAGCATTCAAGATTATTTAGCG 234	
ò	93 LysProLeuArgAspLysIleGlyLysTyrThrSerValGlyThrArgLysGlnProAsn 112	
qq		
λo	113 Leu	
名	259 ATTICCTATGACTIGCCATATGAAGCGGTICTAAAATTIGAACCTGACTTATTATAAIC 318	
ò	127 AspAsnArgHisLysGlylleTyrLysAspLeuAsnLysIleAlaProThr 144	
Ωp	319 AGTICATCTGCTCTAGTIGAAGGCGGTAAATACAAAGAATACAGTAAAATTGCGCCAACT 378	
ζ	AspAlaPhe 16	
QQ	 	
λo	162 LysThrileSerLysAlaLeuGlyLysGluGluGluGlyLystysArgLeuGluGluHis 181	
qa	424 GAAGATATTGCCCCTGTTTTAGATAAAAAGAACAAGCGAAAAAAGTGTTAGAAGATTAT 483	
ò	182 AspLysLyslieGluGluTyrLysLysGluIleThrMetAspLys 196	
qq	484 GATACCTTAACCAAAGGGGTCCAAGAATATCTTGGCAAAAAAGAT 528	
ò	197 AsnGlnLysValLeuProAlaValAlaAlaLysSerGlyLeuLeuAlaHisProSerAsn 216	
qq	529	
.,	217 SerTyrValLeu 226	
qa	 ACTTA 62	
ŏ	227 GlyPheLysGluAlaLeuSerAspNalThrLysGlyLeuSerLysTyrLeuLysGly 246	
equ	625 GGCCTCCAAGTTCCAAAATTAGTGGAAGAAATTTCTAAAAACGCTACTGCG 675	
č	247 ProTyrLeuGlnMetAsnThrGluThrLeuSerGlnValAsnProGluArgMetPhelle 266	
9 90	676 GATIGGAATCAAGTITCTTIAGAAAATTAGCTGAGCTTGACGCAGACCACATITCCTT 735	
7	AsnGluProSerLeuLys	
Db 7	736 GTAAACAGCGATGAATCAGCA	
0y 2	287 TrplysLysLeuAsnAlaValLysAsnGlnArgValAspIleLeuAspArgAspLeuTrp 306	
Db 7	778 TGGAAGAACTTACCTGCTGTGAAAATAACCAAGTTCATACCTATGATAAA 828	
97 3	307 AlaArgSerArgGlyLeulleSerSerGluGluMetAlaLysGluLeuValGluLeuSer 326	

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; Sequence 71, Application US/09071035
; Patent No. 6448043
; GENERAL INFORMATION:
    APPLICANT: Gall H. Choi
    TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
    TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
    TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
    CORRESPONDENCE ADDRESS:
    STREET: 9410 Key West Avenue
    STREET: 945050
    COUNTRY: USA
    STREET: POBSO
    COMPUTER READABLE PORM:
    MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
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|CGGATTATTGCGAGTTATTTAGAA------GATTATCTAGTTGCATTAGGAGAA 145
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26 CysGlyAsn---AsnSerSerSerAsnSerSerLysGluSerSerLysAspGlyValGlu
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Mismatches:
Indels:
Gaps:
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Matches:
                                                                                                                                                                                                                                                                                                                                                             COMPUTER: HF VECTA 30/20
OPERATING SYSTEM: MSDOS Version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
FILING DATE:
CLASSIFICATION :
PRICR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTONNEY AGENT INFORMATION:

NAME: A. Anders Brookes

NEGISTRATION NUMBER: 36,373

REFERENCE/DOCKET NUMBER: PB369P2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8512

TELEPHONE: (301) 309-8512

INPORMATION FOR SEQ ID NO: 71:

SEQUENCE CHARACTERISTICS:

LENGTH: 868 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear
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45.29%
26.76%
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Best Local Similarity:
Query Match:
                                                                           886 AAAAAA 891
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US-09-071-035-71
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Pred. No.:
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                                                                                                                                                230 TATGACTIGCCAIATGAAGCGGTICTAAAAITTGAACCTGACTTATTATTAATCAGTTCA 289
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                                                                                                                                                                                                                                                                                               147 LeulysSerPheAspGlyAspTyrAsnGluAsnIle-----AspAlaPheLysThr 163
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146 AAACCAGTGGCACAATGGACAGTTGGACAAGGCAGCATTCAAGATTATTAGCGAAAGAA 205
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                                       LeuArgAspLys1leGlyLysTyrThrSerValGlyThrArgLysGlnProAsnLeu---
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7 2.1 6202 4 US-09-774-528-120 7 2.1 6270 1 US-08-418-893D-25 7 2.1 6376 4 US-09-949-016-12895 7 2.1 6405 3 US-08-618-016-12895	2.1 6468	2.1 6503	2.1 6527	2.1 7228	2.1 7571	2.1 7826 . 2.1 8436 .	2.1 8855	2.1 8855	2.1 8930	2.1 8954 4 2.1 8968 4	2.1 9039	2.1 9117 4	2.1 9515	2.1 9515 1	2.1 9515	2.1 9515 2	2.1 9581 2	2.1 10711 3	2.1 10758 4	2.1 10772 4	2.1 11073 4	2.1 11258 4 2.1 11831 3	2.1 12055 4	2.1 12223 4	2.1 12687 1	2.1 12687 3 2.1 12687 3	2.1 12865 4	2.1 14333 4	2.1 14467 4	2.1 15492 4 2.1 16378 4	2.1 16741 4	2.1 17245 4	2.1 17503 4	2.1 18048 4	2.1 18049 4 2.1 18551 4	2.1 19068 4	2.1 19181 4 2.1 19181 4	2.1 19296 4	2.1 20441 4	2.1 20713 4 2.1 20727 4	2.1 20727 4	2.1 20728 4	2.1 21048 4 2.1 21295 4

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2705 GGAGTGGAATCAGTGAAGGTTTAAAATTTTAAGTGTAATTGGCTTATTGTTTTA 2764
                                                                                                                                      Sequence 3782, Application US/09710279

Sequence 3782, Application US/09710279

Patent No. 6703492

GENERAL INFORMATION:

APPLICANT: KIMMERLY, WILLIAM JOHN

TITLE OF INVEXTION:

FILE REFERENCE: PU3480US

CURRENT APPLICATION NUMBER: US/09/710,279

CURRENT FILING DATE: 2000-11-09

PRIOR APPLICATION NUMBER: 60/164,258

PRIOR FILING DATE: 1999-11-09

NUMBER OF SEQ ID NOS: 4472

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 3782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
7 OTHER INFORMATION: Description of Artificial Sequence: synthetic
7 OTHER INFORMATION: nucleic acid sequence
1S-09-710-279-3782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2765 ATTGCAACTGCAGCATGTGGAAATAATAGTTCAAGTAACTCAAGT 2809
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US-10-724-972A-6352 (1-335) x US-09-134-001C-2023 (1-183)
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                 148 TTATCTAAGAAAGATAGTAAAAAAGATAATAAG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.46e-26
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Best Local Similarity: 1
Query Match: 1
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US-08-956-171E-2556
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Pred. No.:
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US-09-134-001C-2023

Sequence 2023, Application US/09134001C

Sequence 2023, Application US/09134001C

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: US/09/134,001C
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT PILING DATE: 1998-08-13
PRIOR PILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
SEQ ID NOS: 5674
SUBJECT OF SEQ ID NOS: 5674

SEQ ID NO 2023
LEVEL OF SEQ ID NOS: 5674

LEVEL OF SEQ ID NOS: 5674

LEVEL OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 30, Appl
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Sequence 16910, A
Sequence 12175, A
Sequence 12638, A
Sequence 12637, A
Sequence 14712, A
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Sequence 16739, A
Sequence 16739, A
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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COMPUTER READABLE FORM:

WEDDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-0ct-1997
CLASSIFICATION *CURNOW**
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/09,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 5, 1997
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
APPLICATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: 46,789
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEG ID NO: 2556:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 242 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2556:
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102 TyrThrSerValGlyThrArgLysGlnProAsnLeuGluGlu1leSerLysLeuLysPro 121 247 0000 0000 US-10-724-972A-6352 (1-335) x US-08-956-171E-2556 (1-242) Length:
Matches:
Conservative:
Mismatches:
Indels: 122 AspleuileileAlaAsp 127 1.01e-17 26.00 100.00\$ 100.00\$ 7.76\$ Percent Similarity: Best Local Similarity: Alignment Scores: Pred. No.: Query Match: DB: ઠે a ò

RESULT 4
US-08-781-986A-2556
Sequence 2556 Application US/08781986A
Patent No. 6737298
Harbar Liscontage Sequence 2556 Application US/08781986A
Factor No. 673728
Harbar Liscontage Sequences aureus Polynucleotides and Sequences NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS: ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA

TTD. 20850

COUNTRY. USA
ZIP: 20850
COMPUTER: USA
COMPUTER: READABLE PORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION: <UNKnown>
PRIOR APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INPORMATION:
NAME: Mark J. Hyman

ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:

4 0 0 0 0 0 4 0 US-10-724-972A-6352 (1-335) x US-08-781-986A-2556 (1-242) Length:
Matches:
Conservative:
Mismatches: CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BENBON, BOD
REFERENCE/DOCKET NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELEPHONE: (301) 309-8514
TELEPHONE: (301) 309-8514
INFORMATION FOR SEQ ID NO: 2556:
SEQUENCE CHARACTERISTICS:
LENGTH: 242 base pairs
TYPE: MUCHAEL Caid
STRANDEDNESS: double
STRANDEDNESS: double 1.01e-17 26.00 100.00% 100.00% 7.76% US-08-781-986A-2556 Percent Similarity: Best Local Similarity: Query Match: Alignment Scores: Pred. No.:

102 TyrThrSerValGlyThrArgLysGlnProAsnLeuGluGlulleSerLysLeuLysPro 121 122 AspleuileileAlaAsp 127 ઠે 셤 ò

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RESULT 5
US-08-956-171E-355

US-08-956-171E-355

Sequence 355, Application US/08956171E

Sequence 355, Application US/08956171E

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Tare Application US/08956171E

Sequence 3514

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences UNMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

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Alignment Scores:
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Matches:
Conservative:
Mismatches:
Indels:
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEPHONE: (240) 309-8439
INFORMATION FOR SEQ ID NO: 355:
SEQUENCE CHARACTERISTICS:
LENGTH: 668 base pairs
TYPE: nucleic acid
STAMNEDNESS: double
TYPE: nucleic acid
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Best Local Similarity: 1
Query Match:
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US-08-781-986A-355
                                                                                                                                                                        Alignment Scores:
Pred. No.:
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306 TrpalaargserargGlyLeulleSerSerGluGluMetalarysGluLeuValGluLeu 325
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i Sequence 15, Application US/09830217

parent No. 652141

generat Involvation

i GENERAL INFORMATION:

APPLICANT: Human Genome Sciences, Inc.

TITLE OF INVENTION: Staphylococcus aureus Genes and Polypeptides

TITLE OF INVENTION: PAPPLICATION NUMBER: US/09/830,217

CURRENT APPLICATION NUMBER: US/09/830,217

CURRENT PILING DATE: 1999-0619

PRIOR PILING DATE: 1999-0619

PRIOR PILING DATE: 1998-06-01

PRIOR PILING DATE: 1998-06-01

PRIOR PILING DATE: 1998-06-07

NUMBER: OF SEQ ID NOS: 22

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 15

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; Sequence 15, Application US/10278946
; Patent No. 6821754
; GENERAL INFORMATION:
    APPLICAMY: Simpson et al.
    TITLE OF INVENTION: Staphylococcus aureus Genes and Polypeptides
; TITLE OF INVENTION: Staphylococcus aureus Genes and Polypeptides
; FILE REFERENCE: P8461USD1
; CURRENT APPLICATION NUMBER: US/10/278,946
; PRIOR APPLICATION NUMBER: US 09/830,217
; PRIOR PILING DATE: 2001-04-24
; PRIOR FILING DATE: 1999-03-18
; PRIOR FILING DATE: 1999-03-18
; PRIOR FILING DATE: 1999-03-18
; PRIOR FILING DATE: 1998-03-20
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      Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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; ORGANISM: Staphylococcus aureus
US-09-830-217-15
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Query Match:
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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US-10-278-946-15
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PRIOR APPLICATION NUMBER: US 60/080,296
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: US 60/084,674
PRIOR FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 22
SEQ ID NO 15
LENGTH: 999
COO7 ##.00.00
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Length:
Matches:
Conservative:
Mismatches:
Indels: 8.28e-05 14.00 100.00% 100.00% 4.18% Percent Similarity: Best Local Similarity: Query Match: Alignment Scores:

; TYPE: DNA ; ORGANISM: Staphylococcus aureus US-10-278-946-15

US-10-724-972A-6352 (1-335) x US-10-278-946-15 (1-999)

111 ProAsnLeuGluGluIleSerLysLeuLysProAspLeuIle 124 322 CCTAACTTAGAGGAAATCTCTAAATTAAAACCGGACTTAATT 363 ò 셤

RESULT 9
US-08-956-171E-238
is Sequence 238, Application US/08956171E
is Patent No. 6593114
is GENERAL INFORMATION:
is GENERAL INFORMATION:
is Charles Kunsch
is Patrick S. Dillon
Craig A. Rosen
is Steven C. Barrash
is Steven C. Barrash
is Steven C. Barrash
is Steven C. Barrash
is Steven C. Barrash
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ADDRESSES: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READALE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDGS version 6.2
OCMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDGS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORIZATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: 46,789
REFERENCE/DOCKET NUMBER: 46,789
REFERENCE/DOCKET NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NOW NUMBER: 1224
TELECOMMUNICATION NOW NUMBER: 1224
TELEFAX: (301) 319-1224

INFORMATION FOR SEQ ID NO: 238:
SEQUENCE CHARACTERISTICS:
LENGTH: 3775 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

3775 14 0 0 0 US-10-724-972A-6352 (1-335) x US-08-956-171E-238 (1-3775) Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 0.000295 14.00 100.00% 100.00% Percent Similarity: Best Local Similarity: Query Match: Alignment Scores: Score:

; SEQUENCE DESCRIPTION: SEQ ID NO: 238: US-08-956-171E-238

111 ProAsnLeuGluGluileSerLygLeuLysProAspLeulle 124 ò

RESULT 10
US-08-781-986A-238
US-08-781-986A-238
Sequence 218, Application US/08781986A
Fatent No. 6737248
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION:
TITLE OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER READABLE FORM:

COMPUTER: HP Vectra 486/33
OPERATION SYSTEM: MADOS Version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION 4135
PRIOR APPLICATION 947A:
ATORNEY/AGENT INFORMATION:
ATORNEY/AGENT INFORMATION:
NAME: Beanson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: 9B248PP
TELECOMMUNICATION NUMBER: 9B248PP
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ 1D NO: 238:
SEQUENCE CHARACTERISTICS:
LENGTH: 3775 base pairs

TYPE: nucleic acid STRANDEDNESS: double linear

Length:
Matches:
Conservative:
Mismatches:
Indels: 0.000295 14.00 100.00\$ 100.00\$ Percent Similarity: Best Local Similarity: Query Match: Alignment Scores: Pred. No.:

US-10-724-972A-6352 (1-335) x US-08-781-986A-238 (1-3775)

111 ProAsnLeuGluGluIleSerLysLeuLysProAspLeuIle 124 셤. ò

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US-09-949-016-14517/c
; Sequence 14517, Application US/09949016
; Patent No. 6812339
; Patent No. 6812339
; GENERAL INFORMATION:
    APPLICANT: VENTER, J. Craig et al.
    TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: 60/241, 755
    PRIOR PLILING DATE: 2000-10-20
; PRIOR PLILING DATE: 2000-10-03
; PRIOR PLILING DATE: 2000-10-03
; PRIOR PLILING DATE: 2000-10-03
; PRIOR PLILING DATE: 2000-10-03
; PRIOR PLILING DATE: 2000-10-03
; PRIOR PLILING DATE: 2000-10-03
; PRIOR PLILING DATE: 2000-10-03
; WUMBER OF SEQ ID NOS: 207012
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1 US-09-949-016-14516/c

2 Gequence 14516, Application US/09949016

3 GEQUENCE 14516, Application US/09949016

5 PATEN NO. 681239

5 GENERAL INFORMATION:

1 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

1 TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

1 TITLE OF INVENTION: WINDER: US/09/949,016

5 CURRENT FILING DATE: 2000-04-14

5 PRIOR APPLICATION NUMBER: 60/241,755

6 PRIOR PLING DATE: 2000-10-20

7 PRIOR PLING DATE: 2000-10-20

8 PRIOR FILING DATE: 2000-10-30

8 PRIOR FILING DATE: 2000-09-08

NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER: ESEC ID NOS: 207012

5 SOFTWARE: FastSEQ for Windows Version 4.0

5 SEQ ID NO 14516

LENGTH: 203475
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OTHER INFORMATION: n = A,T,C or G
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NAME/KEY: misc_feature
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ORGANISM: Human
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LENGTH: 203475
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APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTON: FOLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: FOLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: FOLYMORPHISMS: NO FOLSEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

SOFTWARE: FASISEQ for Windows Version 4.0

SEQ ID NO 14230

LEMEGTH: 13248
              US-09-949-016-12024/c
US-09-949-016-12024/c
Sequence 12024, Application US/09949016
Factor 12024, Application US/09949016
Factor No. 681239
GENERAL INPORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES OF OLS
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
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Mismatches:
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108-09-949-016-14230/c
108-09-949-016-14210, Application US/09949016
; Patent No. 6812339
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Best Local Similarity:
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Best Local Similarity:
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US-09-949-016-12024
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Pred. No.:
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US-10-724-972A-6352 (1-335) x US-09-949-016-14519 (1-203475)
             PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FESTS FOR Windows Version 4.0
SEQ ID NO 14519
LENGTH: 203475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67872 AGCAACTCCTCCCAAGGAGGTCTAAG 67846
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                                                                                                                                                                                                                        FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(203475)

OTHER INFORMATION: n = A,T,C or
US-09-949-016-14519
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Best Local Similarity:
Query Match:
                                                                                                                                                                                    TYPE: DNA
ORGANISM: Human
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ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                                                               Score:
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Sequence 14518, Application US/09949016

Facent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-00-01-1

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-00-08

NUMBER OF SEQ ID NOS: 207012

SOCTHARE: PSELSEQ for Windows Version 4.0

SEQ ID NO 14518

LENGTH: 203475
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US-09-949-016-14519/C

i Sequence 14519, Application US/09949016

i Sequence 14519, Application US/09949016

i Patent No. 6812339

i GENERAL INFORMATION:

i APPLICANT: VENTER, J. Craig et al.

i TILLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

i TILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

i TILLE OF INVENTION: WINMER: US/09/949, 016

i CURRENT FILING DATE: 2000-04-14

i PRIOR APPLICATION NUMBER: 60/241,755
                                                                                                    203475
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                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
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; LOCATION: (1)...(201475)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14517

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; LOCATION: (1)...(201475)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14518
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Best Local Similarity:
Query Match:
DB:
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FEATURE:
                                                                              Alignment Scores:
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Pred. No.:
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Conservative: Mismatches: Indels:

Gaps:

Length: Matches:

1.82e+03 9.00 100.00% 100.00% 2.69%

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ABOUT 17226/C

Sequence 17226, Application US/09949016

Patent No. 681239

HIGHERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASTSEQ for Windows Version 4.0

LENGTH: 203475
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Matches:
Conservative:
Mismatches:
Indels:
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i LOCATION: (1)...(203475)
CTHER INFORMATION: n = A,T,C or G
US-09-949-016-17226
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Best Local Similarity:
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= A, T, C or G
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; LOCATION: (1)...(203475);
; OTHER INFORMATION: n = P
US-09-949-016-17229
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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Alignment Scores:
Pred. No.:
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## Sequence 1728 Application US/09949016

## Sequence 1728 Application US/09949016

## Sequence 1728 Application US/09949016

## APPLICANT: VENTER, J. Craig et al.

## TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

## TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

## TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

## TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

## TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

## PRIOR APPLICATION NUMBER: 60/231,768

## PRIOR PILING DATE: 2000-10-20

## PRIOR PILING DATE: 2000-10-03

## PRIOR PILING DATE: 2000-10-03

## PRIOR PILING DATE: 2000-09-08

## NUMBER OF SEQ ID NOS: 207012

## SEQ ID NO 17228

## LENGTHARE: FREETED for Windows Version 4.0

## SEQ ID NO 17228
                                                                  Sequence 17227, Application US/09949016

j Sequence 17227, Application US/09949016

j Batent No. 6812339

j GENERAL INFORMATION:
    APPLICANT: VENTER, J. Craig et al.
    APPLICANT: VENTER, J. Craig et al.
    ITLE OF INVENTION: MITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
    TITLE OF INVENTION: MITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
    TITLE OF INVENTION: MITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
    TITLE OF INVENTION: MITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
    TITLE OF INVENTION: MITH HUMAN DISEASE, METHODS OF DETECTION AND USER: 2000-04-14
    PRIOR APPLICATION NUMBER: 60/231,768
    PRIOR FILING DATE: 2000-10-20
    PRIOR APPLICATION NUMBER: 60/231,768
    PRIOR PILING DATE: 2000-10-03
    PRIOR PILING DATE: 2000-10-03
    PRIOR APPLICATION NUMBER: 60/231,498
    NUMBER OF SEQ ID NOS: 207012
    SEQ ID NO 17227
    LENGTH 203475
    LENGTH: 203475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-724-972A-6352 (1-335) x US-09-949-016-17227 (1-203475)
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION; (1) ... (203475)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17227
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// LOCATION: (1)...(203475)

// OTHER INFORMATION: n = A,T,C or

// US-09-949-016-17228
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Best Local Similarity:
Query Match:
DB:
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US-09-949-016-17228/c
                                                                -016-17227/c
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ORGANISM: Human
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US-09-949-016-17229/c

US-09-949-016-17229/c

Sequence 17229, Application US/09949016

Sequence 17229, Application US/09949016

GENERAL INFORMATION:
TITLE OF INVENTION: DOLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: US/09/949,016

TITLE OF INVENTION: UNMER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRASESQ for Windows Version 4.0

SEQ ID NO 17229
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US-09-513-999C-32507/C
; Sequence 32507, Application US/09513999C
; Sequence 32507, Application US/09513999C
; Patent No. 6783961
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Glordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; PATENT NO. 6783961
; PRIDE REPERBUCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 1209-0-22.44
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR PILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-724-972A-6352 (1-335) x US-09-949-016-17229 (1-203475)
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Conservative:
Mismatches:
    Length:
Matches:
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Mismatches:
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                                                                                                                             Gaps:
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GENERAL INCORMATION:
GENERAL INCORMATION:
APPLICANT: Dumas Milline Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
APPLICANT: Glordano, J.Y.
ITILE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NOS: 36681
SEQ ID NOS: 36681
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Matches:
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Mismatches:
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; Sequence 29145, Application US/09513999C
; Patent No. 6783961
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; LOCATION: 50
: OTHER INFORMATION: Xaa=ABP or Glu
US-09-513-999C-2950
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LOCATION: 119
OTHER INFORMATION: s=g of
FEATURE:
NAME/KEY: misc_feature
LOCATION: 121
OTHER INFORMATION: s=g of
FEATURE:
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LOCATION: 188
COTHER INFORMATION: m=a or
FEATURE:
NAME/KEY: misc_feature
LOCATION: 189
OTHER INFORMATION: s=g or
                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: misc feature
LOCATION: 260
OTHER INFORMATION: v=a
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LOCATION: 111..350
FEATURE:
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Best Local Similarity:
Query Match:
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LOCATION: 27
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Sequence 5824, Application US/09313294A

Sequence 5824, Application US/09313294A

Sequence 5824, Application US/09313294A

SERENCAL INFORMATION:

APPLICANT: Lalgudi, Raghunath V.

APPLICANT: Low. Laura Y.

APPLICANT: Sherman, Bradley K.

TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR FILE REFERENCE: PL-0017 US

CURRENT APPLICATION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR FILE REFERENCE: 1999-05-14

NUMBER OF SEQ ID NOS: 7600

SSOFTWARE: PREL PROGram

SEQ ID NO 5824

LENGTH: 305
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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US-09-513-999C-2950
; Sequence 2950, Application US/09513999C
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2.39%
SOFTWARE: Patent.pm
SEQ ID NO 32507
LENGTH: 181
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 16
OTHER INFORMATION: r=a OF
FEATURE:
NAME/KEY: misc_feature
LOCATION: 130
OTHER INFORMATION: 8=g OF
FEATURE:
NAME/KEY: misc_feature
LOCATION: 130
OTHER INFORMATION: 8=g OF
FEATURE:
NAME/KEY: misc_feature
LOCATION: 131
COUNTY.
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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ORGANISM: Zea mays
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Pred. No.:
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USOULY 2/
USO9-99-016-39108

Sequence 39108, Application US/09949016

Sequence 39108, Application US/09949016

Sequence 39108, Application US/09949016

SEQUENCE INCOMPATION: DOLYMORHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: POLYMORHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09

NUMBER OF SEQ ID MOS: 207012

SEQ ID NOS: 207012

SEQ ID NO 39108

TENNOM: 207012
 APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REPERREC: 38-10(15849)B
CURRENT APPLICATION NUMBER: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 2334
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Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
Indels:
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| ORGANISM: Myxococcus xanthus |
| PEATURE: | NAME/KEY: unsure |
| LOCATION: (1)..(564) |
| LOCATION: (1)..(564) |
| US-09-902-540-2334 |
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Query Match:
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ORGANISM: Human
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Pred. No.:
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US-09-238-352-884
US-09-238-352-884
US-09-238-352-884
Squence 844, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NOS: 8252
LENGTH: 390
APPLICANT: Dunas Mills Edwards, J.B.
APPLICANT: Dunas Mills Edwards, J.B.
APPLICANT: Dunas Mills Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Fatent No. (78395159-122.REG
CURRENT FILING DATE: 2000-02-24
FRIOR PRILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 29145
LENGTH: 378
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US-09-902-540-2334
Sequence 2334, Application US/09902540
; Patent No. 6833447
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, ORGANISM: Acinetobacter baumannii
US-09-328-352-884
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) LOCATION: 271

) OTHER INFORMATION: m=a or c

US-09-513-999C-29145
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ORGANISM: Homo sapiens
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Best Local Similarity:
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RESULT 30

US-09-949-016-135038

Sequence 135038, Application US/09949016

Sequence 135038, Application US/09949016

Setent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER,
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFREENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 135038
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Sequence 149234, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FREYSEQ for Windows Version 4.0

SEQ ID NO 149234

LENGTH: 601
                                   US-10-724-972A-6352 (1-335) x US-09-949-016-60204 (1-601)
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
Query Match:
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; ORGANISM: Human
US-09-949-016-135038
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US-09-949-016-149234
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                                                      US-09-949-016-60203/c

Sequence 60203, Application US/09949016

Sequence 60203, Application US/09949016

Fatent No. 6812339

Fatent No. 681239

FILE OF INVENTION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

FRIOR FILING DATE: 2000-10-20

FRIOR FILING DATE: 2000-10-20

FRIOR FILING DATE: 2000-10-30

FRIOR FILING DATE: 2000-09-08

NUMBER: 0F SEQ ID NOS: 207012

SEQ ID NO 60203

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Batent No. 681239
GENERAL INFORMATION:
TOTAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUWAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
FILE REFERENCE: 2000-04-14
FRICH RAPLICATION NUMBER: 60/231,768
FRICH RILING DATE: 2000-10-20
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTHARE: FBSESEQ for Windows Version 4.0
SEQ ID NO 62204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-724-972A-6352 (1-335) x US-09-949-016-60203 (1-601)
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Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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69 GAAGAAGAGGAAAAAAAAAGACTC 92
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Best Local Similarity:
Query Match:
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US-09-949-016-60204/c

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; TYPE: DNA ; ORGANISM: Human US-09-949-016-60203

Alignment Scores:

Percent Similarity: Best Local Similarity: Query Match: DB:

; TYPE: DNA ; ORGANISM: Human US-09-949-016-60204

Alignment Scores:

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Sequence 1850, Application US/09543681A
Sequence 1850, Application US/09543681A
Patent No. 6605709
GENERAL INPORMATION:
TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILL)
TITLE OF INVENTION: UNCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: UNMERS: US/09/543,681A
FILE REFERENCE: 2709.1002-001
FILE REFERENCE: 2709.1002-001
CURRENT FAPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 1850
LENGTH: 843
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GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 14140
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; Patent No. 6703491
                                                                                                                                       24 AlaAlaCysGlyAsnAsnSerSer 31
                                                                                                                                                          46 GCAGCCTGTGGCAACAATTCATCT 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-14140
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8.00
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; ORGANISM: Proteus mirabilis
US-09-543-681A-1850
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Query Match:
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US-09-270-767-14140
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US-09-134-001C-909
i Sequence 909, Application US/09134001C
j Patent No. 6380370
general information:
    Application US/09134001C
j Patent No. 6380370
general information:
    Application US/09134001C
j Patent No. 6380370
i TITLE OF INVENTION:
    ATTLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
    TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
    TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
    CURRENT FILING DATE: 1998-08-13
    PRIOR FILING DATE: 1998-08-13
    PRIOR APPLICATION NUMBER: US 60/064,964
    PRIOR FILING DATE: 1997-11-08
    PRIOR FILING DATE: 1997-11-08
    NUMBER OF SEQ ID NOS: 5674
    SEQ ID NO 909
    LENGTH: 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1567, Application US/09710279

Sequence 1567, Application US/09710279

Patent No. 6703492

GENERAL INFORMATION:
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS

TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS

FILE REPERENCE: PUJ480US

CURRENT APPLICATION NUMBER: 0200-11-09

PRIOR PILING DATE: 1999-11-09

NUMBER OF SEQ ID NOS: 4472

SOFTWARE: PATENT VET. 2.1

SEQ ID NO 1567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
COTHER INFORMATION: Description of Artificial Sequence: synthetic
FEATURE INFORMATION: nucleic acid sequence
CS-09-710-279-1567
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Matches:
Conservative:
Mismatches:
Indels:
                            Conservative:
Mismatches:
Indels:
              Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
, ORGANISM: Staphylococcus epidermidis
US-09-134-001C-909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46 GCAGCCTGTGGCAACAATTCATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity:
Query Match:
DB:
                            Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-09-710-279-1567
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Pred. No.:
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B-10-/24-9/28-0352.011go.rni
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RESULT 38

US-09-641-638-193

i Sequence 193, Application US/09641638

patent No. 6432648

GENERAL INFORMATION:
APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
APPLICANT: Cohen, Annick
TITLE OF INVENTION: BLALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
TITLE OF INVENTION: BLALLELIC MARKERS DERIVED FROM GENOMIC REGIONS
TITLE OF INVENTION: GENEE: US/09/641,638

FILE REFERENCE: GENSET.051CP1
CURRENT FILING DATE: 2000-08-16
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR FILING DATE: 1999-05-07
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 1304
SEQ ID NO 193
HENGTH: 1001
HENGTH: 1001
              NAME/KEY: misc_binding
| IOCATION: 202. 521
| O'THER INPORMATION: 12-515-394.mis2, potential complement
| IOCATION: 107.126
| O'THER INPORMATION: upstream amplification primer
| IOCATION: 107.126
| O'THER INPORMATION: upstream amplification primer
| IOCATION: 537.1557
| O'THER INFORMATION: downstream amplification primer, complement
| NAME/KEY: pinding
| IOCATION: 489.513
| O'THER INFORMATION: 12-515-394 potential probe
| US-09-641-638-192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc binding LOCATION: 502. 520
OTHER INFORMATION: 12-516-97.mis2, complement
NAME/KEY: primer bind
OTHER INFORMATION: upstream amplification primer
NAME/KEY: primer bind
LOCATION: 891..91
OCATION: 891..91
OCATION: MANE/KEY: primer bind
LOCATION: MANE/KEY: primer with the primer complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: allele
LOCATION: 501
OTHER INFORMATION: 12-516-97 : polymorphic base C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-724-972A-6352 (1-335) x US-09-641-638-192 (1-1001)
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
OTHER INFORMATION: 12-515-394.mis1, potential
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ORGANISM: Homo Sapiens
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Best Local Similarity:
Ouery Match:
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Pred. No.:
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APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 2246
LENGTH: 981
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US-09-641-638-192

Sequence 192. Application US/09641638

Petent No. 6432648

GENERAL INFORMATION:
APPLICANT: Blumenfeld, Marta
APPLICANT: Bouqueleret, Lydie
APPLICANT: Bouqueleret, Lydie
APPLICANT: Cohen, Annick
TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS
TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS
TITLE OF INVENTION: GENEET 051CP1
CURRENT APPLICATION NUMBER: US/09/641,638
CURRENT APPLICATION NUMBER: US 60/133,200
PRIOR PELING DATE: 1090-02-11
PRIOR PELING DATE: 1999-03-23
PRIOR FILING DATE: 1999-03-23
PRIOR FILING DATE: 1999-03-23
PRIOR PELING DATE: 1999-02-12

PRIOR PELING DATE: 1999-02-12

PRIOR PELING DATE: 1999-02-12

NUMBER OF SEQ ID NOS: 1304

SOFTWARE: Patent.pm
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NAME/KEY: allele
LOCATION: S01
OTHER INFORMATION: 12-515-394 : polymorphic base A or T
NAME/KEY: misc_binding
LOCATION: 481..500
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Matches:
Conservative:
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Indels:
28 AsnAsnSerSerAsnSerSer 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              678 GCCGTGGCTGCAAAAGCGGACTG 701
                                                                                                                                      Sequence 2246, Application US/09489039A
Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
CRGANISM: Klebsiella pneumoniae
US-09-489-039A-2246
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ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
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Pred. No.:
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LENGTH: 1001
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NSENDLY 40
US-10-170-097-193

| Sequence 193, Application US/10170097
| Patent No. 6794143
| Patent No. 6794143
| Patent INCORMATION:
| APPLICANT: Blumenfeld, Marta
| APPLICANT: Blumenfeld, Marta
| APPLICANT: Cohen, Annick
| TITLE OF INVENTION: BLALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
| TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
| TITLE OF INVENTION: GEN-T1144XC2D1
| TITLE OF INVENTION: GEN-T1144XC2D1
| TITLE OF INVENTION: GEN-T1144XC2D1
| FILE REPERENCE: GEN-T1144XC2D1
| CURRENT APPLICATION NUMBER: US/10/170,097
| CURRENT FILING DATE: 2000-06-10
| PRIOR FILING DATE: 2000-06-10
| PRIOR FILING DATE: 2000-06-10
| PRIOR FILING DATE: 1999-05-07
| PRIOR FILING DATE: 1999-05-07
| PRIOR FILING DATE: 1999-05-07
| PRIOR FILING DATE: 1999-03-13
| PRIOR FILING DATE: 1999-03-13
| PRIOR FILING DATE: 1999-03-12
| PRIOR FILING DATE: 1999-03-12
| PRIOR FILING DATE: 1999-02-12
| PRIOR FILING DATE: 1999-02-12
| PRIOR FILING DATE: 1999-02-12
| PRIOR FILING DATE: 1999-03-13
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LOCATION: 891..911
OTHER INFORMATION: downstream amplification primer, complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: allele
LOCATION: 501
OTHER INFORMATION: 12-516-97 : polymorphic base C or T
FEATURE:
NAME/KEY: misc binding
LOCATION: 481..500
OTHER INFORMATION: 12-516-97.misl, potential
                                                                                                                                                                                                                                                                                                                                          US-10-724-972A-6352 (1-335) x US-10-170-097-192 (1-1001)
                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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LOCATION: 405..424
OTHER INFORMATION: upstream amplification primer
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LOCATION: 502..520
OTHER INFORMATION: 12-516-97.mis2, complement
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   923 AATTCTAGCTCTAACAGCTCTAAA 946
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ORGANISM: Homo Sapiens
                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
                                                                  Alignment Scores:
Pred. No.:
US-10-170-097-192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 192, Application US/10170097

Sequence 192, Application US/10170097

Patent No. 6794143

GENERAL INFORMATION:

APPLICANT: Blumenfeld, Marta

APPLICANT: Blumenfeld, Marta

APPLICANT: Cohen, Annick

TITLE OF INVENITON: BILLELIC MARKERS DERIVED FROM GENOMIC REGIONS

TITLE OF INVENITON: BALLELIC MARKERS DERIVED FROM GENOMIC REGIONS

TITLE OF INVENITON: BALLELIC MARKERS DERIVED FROM GENOMIC REGIONS

TITLE OF INVENITON: BALLELIC MARKERS DERIVED FROM GENOMIC REGIONS

TITLE OF INVENITON: BALLELICE MARKERS DERIVED FROM GENOMIC REGIONS

TITLE OF INVENITON: BALLELICE MARKERS DERIVED FROM GENOMIC REGIONS

FILE REFERENCE: GEN-TI14XC2D1

FILE REFERENCE: GEN-TI14XC2D1

FILE REFERENCE: GEN-TI14XC2D1

FILE REFERENCE: GEN-TI14XC2D1

FRIOR FILING DATE: 2000-06-10

FRIOR FILING DATE: 1099-05-07

FRIOR FILING DATE: 1999-03-13

FRIOR FILING DATE: 1999-03-13

FRIOR FILING DATE: 1999-03-12

FRIOR FILING DATE: 1999-03-12

FRIOR FILING DATE: 1999-02-12

FRIOR FILING DATE: 1999-02-12

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LOCATION: 537..557
OTHER INFORMATION: downstream amplification primer, complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KRY: misc_binding
LOCATION: 502..521
OTHER INFORMATION: 12-515-394.mis2, potential complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: 12-515-394 : polymorphic base A or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-724-972A-6352 (1-335) x US-09-641-638-193 (1-1001)
                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
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LOCATION: 107..126
OTHER INFORMATION: upstream amplification primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEX: misc_binding
LOCATION: 481.500
OTHER INFORMATION: 12-515-394.misl, potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      // NAME/KEY: misc_binding
// LOCATION: 489..513
// OTHER INFORMATION: 12-516-97 potential probe
US-09-641-638-193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 717 AATTCTAGCTCTAACAGCTCTAAA 740
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                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: allele
LOCATION: 501
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US-10-170-097-192
                                                                                                                                                                                                  Alignment Scores:
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Length: Matches: Conservative: Mismatches: Indels:	10-170-097-193 (1-1001	erLyB 36 CTAAA 740
121 8.00 100.00% 100.00% 2.39%	335) x US-1	AsnSerS AACAGCT
Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match:	US-10-724-972A-6352 (1-335) x US-10-170-097-193 (1-1001)	Oy 29 AenSerSerSerAenSerSerLye 36
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Search completed: November 10, 2005, 03:07:59 Job time : 664 secs

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AE016750 300698 bp DNA linear BCT 01-JAN-2003 Staphylococcus epidermidis ATCC 12228, section 7 of 9 of the
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Staphylococcus epidermidis ATCC 12228
Bacteria; Firmicutes; Bacillales; Staphylococcus.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
Candy.Y., Ren.S., Li,H., Fu,G., Lu,L., Lu,G., Jia,J., Tu,Y., Din,Z., Chen,Z. and Wen,Y.
Direct Submission
Submitted (05-NOV-2002) Chinese National Human Genome Center at Shanghai, 250 Bl Bo Road, Shanghai 201203, China Location/Qualifiers
I. 310698
I. 310698
| Coganism=Staphylococcus epidermidis ATCC 12228" | Mol type="genomic DNA" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 12228" | Atrain="ATCC 122
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DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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JOURNAL
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-MODEL=frame+_D2n.model -DEV=x1h
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-NOW TIMEOUT=310 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                                                                                                                                                                     2005, 19:43:37 ; Search time 5171 Seconds (without alignments) 3139.141 Million cell updates/sec
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              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                               - nucleic search, using frame plus p2n model
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0 , Ygapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 2000000000
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Match Length DB
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AX583941 Sequence BD237137 Staphyloc AR282355 Sequence AF079518 Staphyloc AR354120 Sequence

Continuation (34 o

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AP003136 BA000018
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Cui,L., Oguchi,A., Aoki,K., Nagai,Y., Lian,J., Ito,T., Kanamori,M.,
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Sekimizu,K., Hirakawa,H., Kuhara,S., Goto,S., Yabuzaki,J.,
Kanehisa,M., Yamaahita,A., Oshima,K., Furuya,K., Yoshino,C.,
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Whole genome sequencing of meticillin-resistant Staphylococcus
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On Jun 12, 2001 this sequence version replaced gi:13701842.
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Director-General, Biotechnology Center, Aoki,K., Oguchi,A.,
Hosoyama,A., Nagai,Y., Kuroda,M., Hiramatsu,K. and Kikuchi,H.
Direct Submission
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Best Local Similarity:
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Pred. No.:
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small subunit"
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protein MutS"
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Kuroda, M., Ohta, T., Uchiyama, I., Baba, T., Yuzawa, H., Kobayashi, I., Cui, L., Oguchi, A., Aoki, K., Nagai, Y., Lian, J., Ito, T., Kanamori, M., Matsumaru, H., Macyoyama, A., Murakami, H., Hosoyama, A., Mizutami - Ui, Y., Takahashi, N. K., Sawano, T., Inoue, R., Kaito, C., Sekimizu, K., Hirakawa, H., Kuhara, S., Goto, S., Yabuzaki, J., Kanehisa, M., Yamashita, A., Oshima, K., Furuya, K., Yoshimo, C., Shiba, T., Hattori, M., Osasawara, N., Hayashi, H. and Hiramatsu, K., Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      On Apr 16, 2004 this sequence version replaced gi:14247707.
This work was done in collaboration with Toshiko Ohta, Mutsumi Kanamori, Hideo Hayashi (University) of Tsukuba), Hideki Hirakawa, Satoru Kuhara (Kyushu University), Ikuo Uchiyama (Okazaki National University), Naotake Ogasawara (Nara Institute of Science and Technology) and supported by the Research for the Future Program of the Japan Society for the Promotion of Science.
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Nucleotide Substitutions in Staphylococcus aureus Strains, MuSO, Mu3, and N315
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Hattori, M., Yamashita, A., Oshima, K. and Shiba, T.
Birect Submission
Submitted (28-FEB-2001) Masahira Hattori, Kitasato Institute for Life Sciences, Kitasato University; Kitasato 1-15-1, Sagamihara, Kanagawa 228-855, Japan
(E-mail:hattoriagenome.ls.kitasato-u.ac.jp, Tel:81-42-778-8194,
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Staphylococcus aureus subsp. aureus Mu50
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/ locus tag="SAV1938"

complement (2027 . 3457)

/ locus tag="SAV1938"

/ locus tag="SAV1938"

/ note="Bacteriophage phi Sa 3mu"

/ note="Bacteriophage phi Sa 3mu"

/ codon start=1

/ transl_table=11

/ product="trucated map-w protein"

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/ protein id="Bab58100.1"

/ protein id="Bab58100.1"

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SYTITVNGTSQNILSNLTPRKOQNISYCLEGKVKXSVLESNRGITDVDLKLSKQAKYT

WNFKNGTKKVIDLKSGIYTANLINSSDIKSINIVWTGTKAKANYQVYSYSINLN

GTSGNILSNLSNLSRUSKWTANLVSHAKNOVKRIETTSQHKANAPYTTANNGTSPPILSKLK

ISNKQLISYKYLNDKVKSVLKSERGISDLDKFAKQAKYTVYFKNGKQVVNLKSDIF

TPNLESAKDIKTDIDVKQYTKSKKK"

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/protein id="BABSS101.2"
/db_xrefe="G1:4639539"
/translation="WHLFCCKLYKRSDNDGKKTKSNSLKKVATLALANLLLVGALTDNSAKAESKKDDTDLKLVSHNVYMLSTVLYPNWRLLT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QTYPIFDKDGHYTTDSLYALLOSYNDDKYIMILNY PRNPTGYTPTHKEVTTIVDAIKA

QTYPIFDKDGHYTTDSLVEALQSYNDDKYIMILNY PRNPTGYTPTHKEVTTIVDAIKA

GTYPIFDKDGHYTTDSLVEALQSYNDDKYIMILNY PRNPTGYTPTHKEVTTIVDAIKA

RVGFWTFGTSDGTTKEVLEAKVYGLFTRSNISSGPLPTQSAVKHYLKNNRQFDKEIEQN

IQTLKERYEVTYKEVVYADQYHSHWQAYDFNSGYFMAIKVHDVDPEELRKHLIEKYSIG

COMPLEMENT (1722. . 2042)

Alocus Laga-SAV1937.

Alocus Laga-SAV1937.

Alocus Laga-SAV1937.

Alocus = "Bacteriophage phi Sa 3mu"
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/protein_id="BAB58098.1"
/protein_id="BAB58098.1"
/db_xxef="d1:14247109"
/translation="MMPLAQSINEDLOQSNATAFTMLSDLGQNMFYPKGILSOSAEAK
STTYNATIGMATNACOGKHEASELDAMPNDLTPDEIFPYAPPQGIEELRDLWQQKMLRD
NPELSIDNMSLPIVTNALTHGLSLVQDLFVNQDLFVNGTNAGANL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="wkkkinksnnvkepvtinkfenivsnefvpynaskitindlsik
Lksamandggitkhdiglaeravykvyfkngsskyvdlkteykdervfkatdikkvdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    product="truncated map-w protein"
protein id="BAB58099.1"
db_xref="G1:14247710"
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/note="Bacteriophage phi Sa 3mu"
/codon_start=1
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/gene="truncated-hlb"
/locus tag='SAV1939"
/note="Bacteriophage phi Sa 3mu"
                                                                                 /sub_species="aureus Mu50"
/db_xref="taxon:158878"
             /mol_type="genomic DNA"
/strain="Mu50"
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/gene="truncated-hlb"
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transl_table=11
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238402 GAACTTGTTGAATTATCAAAAAAAAAAAAAA 238370

GlubeuValGlubeuSerLysLysAspSerLys 331

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LeuAspArgAspLeuTrpAlaArgSerArgGlyLeuIleSerSerGluGluMerAlaLys

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Matches:
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                     HisaspLysLysIleGluGluTyrLysLysGluIleThrMetAspLysAsnGlnLysVal
                                                                 IleAlaProThrIleGluLeuLysSerPheAspClyAspTyrAsnGluAsnIleAspAla
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· · · · · · · · · · · · · · · · · · ·	RESULT 6 AP004829/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL MEDLINE	PUBMED REFERENCE AUTHORS TITLE JOURNAL FEATURES . SOURCE	gene	gene

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Matches:
Conservative:
Mismatches:
Indels:
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1.47e-80
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	_	ORGANISM Staphylococcus aureus REFERENCE 1 AUTHORS Masignani, V.C., Mora, M.C. and Scarselli, M.C. TITLE Staphylococcus aureus proteins and nucleic acids JOURNAL Patent: WO 02094868-A 5331 28-NOV-2002; Chiron Spa (IT) FEATURES Location/Qualifiers Aurioration/Qualifiers Aurioration/Qualifiers Aurioration/Qualifiers Aurioration/Qualifiers Aurioration/Qualifiers Aurioration/Qualifiers Aurioration/Cualifiers Aurioration/Cualifiers Aurioration/Cualifiers Aurioration/Cualifiers	ORIGIN Alignment Scores: Alignment Scores: Pred. No.: Score: 1.83e-82 Matches: Percent Similarity: 84.59\$ Conservative: Query Match: 71.60\$ Mismatches: 11.83\$ Indels: 2	Gaps: 0 Gaps	

BCT 20-DEC-2002

DNA, complete genome

Oguchi, A.,

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Nagai, Y., Asano, K., Iwama, N., Baba, T., Kuroda, M., Hiramatsu, K. and
                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (06-MAR-2002) Director-General, Biotechnology Center, National Institute of Technology and Evaluation, Biotechnology Center; 2Chome 49-10 Nishihara, Shibuya-ku, Tokyo 151-0066, Japan (B-mail:bio@mite.go.jp, URL:http://www.bio.nite.go.jp/, Tel:81-3-3481-1933, PAR:81-3-3481-8424)
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Yamamoto,K. and Hiramatsu,K.
Genome and virulence determinants of high virulence
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Staphylococcus aureus subsp. aureus MW2
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Conservative:
Mismatches:
Indels:
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Cistem Biotechnologies GmbH (AT)
Location/Qualifiers
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173 GluGlyLysLysArgLeuGluGluHisAspLysIleGluGluTyrLysLysGluIle 192 ::		AP003132 Staphylococcus aureus subsp. aureus N315 genomic DNA, compl genome, section 4/10. AP003132 BA000018 AP003132.2 GI:14349174 Staphylococcus aureus subsp. aureus N315 Staphylococcus aureus subsp. aureus N315 Bacteria: Firmicutes: Bacillales: Staphylococcus	l. Kuroda, M., Ohta, T., Uc Cui, L., Oguchi, A., Aob Matsumaru, H., Maruyama Mizutani-Ui, Y., Takaha Sekimizu, K., Hirakawa, Kanehisa, M., Yamashica Shiba, T., Hattori, M., Whole genome sequencir aureus Lancet 357 (9264), 122 21311952	O
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        On Apr 15, 2004 this sequence version replaced gi:14246761.
This work was done in collaboration with Toshiko Ohta, Mutsumi Kanamori, Hideo Hayashi (University of Tsukuba), Hideki Hirakawa, Satoru Kuhara (Kyubahu University), Ikuo Uchiyama (Okazaki National Research Institutes), Susumu Goto, Minoru Kanehisa (Kyoto University), Naocake Ogasawara (Nara Institute of Science and Technology) and supported by the Research for the Future Program of the Japan Society for the Promotion of Science.
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Shiba,T., Hattori,M., Ogasawara,N., Hayashi,H. and Hiramatsu,K.Whole genome sequencing of meticillin-resistant Staphylococcus
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Hattori, M. Yamaahita, A., Oshima, K. and Shiba, T.

Direct Submission

Submitted (18-FEB-2001) Masahira Hattori, Kitasato Institute for Life Sciences, Kitasato University; Kitasato 1-15-1, Sagamihara, Kanagawa 228-8555, Japan

(E-mail:hattorigenome.ls.Kitasato-u.ac.jp, Tel:81-42-778-8194,
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Yamashita,A., Oshima,K., Kuroda,M., Hattori,M., Hiramatsu,K.,
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                                                                                                                                                                                                     291 AsnalayaliyyaAsnGlnArgyalAspIleLeuAspArgAspLeuTrpAlaArgSerArg
                                                                                                                         SerSerAsnGluProSerLeuLysGluLeuGluLysAspPro---ValTrpLysLysLeu
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aureus Mu50 DNA, complete genome
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Staphylococcus aureus subsp. aureus Mu50
Bacteria; Firmicutes; Bacillales; Staphylococcus.
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DNA RESEARCH 11, 51-56 (2004)
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CGSSFRTAKVAGNPENC"
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PATENT: WO 9731114-A 10 28-AUG-1997;
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                                                                                                                     ValileGlyLeuLeuPheValLeuIleAlaThrAlaAlaCysGlyAsnAsnSerSerSer
                                                                                                                                              AsnSerSerLysGluSerSerLysAspGlyValGlullelysHisGluGluGlyThrThr
                                                                                                                                                                                   LysProLeuArgAspLysIleGlyLysTyrThrServalGlyThrArgLysGlnProAsn
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|46582 AAAATCAAAATTGAGCAAAATTGCTCCGACAATCATGTTAGCGGTACGGGA
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                           Length:
Matches:
Conservative:
Mismatches:
                                                                                       US-10-724-972A-6352 (1-335) x AP003361 (1-347785)
complement (10061. .10846)
                         1.24e-42
724.50
66.67$
46.86$
                                        Percent Similarity:
Best Local Similarity:
Query Match:
              Alignment Scores:
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                                                                                                      GluGlyLysLysArgLeuGluGluHisAspLysLleGluGluTyrLysLysGluIle
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                                                                             of
                             bj Rnvad,M.E., j Rgensen,P.L. and Hansen,P.K.
Homologous recombination into bacterium for the generation
polynucleotide libraries
Patent: WO 03095658-A 20 20-NOV-2003;
Novozymes A/S (DK)
Location,Qualifiers
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Bacillus subtilis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
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Sequence 20 from Patent W003095658.
AX951891 GI:40782280
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                                                                           TGCTGAGCATGATAAATTAATCAATAAGTATAAAGATGAAATTAAATTTGATAGAAATCA
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Best Local Similarity:
Query Match:
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BX571856 00
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367 TTTACACACGCTGTGAAGTCAGAT-----AACGCC
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region,
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                                  167
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Bacillus subtilis
Bacillus subtilis
Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yamamoto, H., Uchiyama, S., Nugroho, F.A. and Sekiguchi, J. Cloning and sequencing of a 35.7 kb in the 70 degree-73 degree region of the Bacillus subtilis genome reveal genes for a new two-component system, three spore germination proteins, an iron uptake system and a general stress response protein Gene 194 (2), 191-199 (1997)
Sekiguchi, J.
Sekiguchi, J.
Sekiguchi, J.
Direct Submission
Submitted (09-JUL-1996) Junichi Sekiguchi, Textile Science and Technology, Shinshu University, Department of Applied Biology; 3-15-1 Tokida, Ueda-shi, Nagano 386, Japan
(E-mail:jsekiguggiptc.shinshu-u.ac.jp, Tel:0268-21-5344,
                                                                       ArgSerArgGlyLeulleSerSerGluGluMetAlaLysGluLeuValGlu 324
                                                                                                  DNA linear
DNA, 70-73 degree
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The complete genome sequence of the gram-positive bacterium Bacillus subtilis
Nature 390 (6657), 249-256 (1997)
Bacillus subtilis subsp. subtilis str. 168
Bacillus subtilis subsp. subtilis str. 168
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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This entry contains data from release R16.1 of the SubtiList database. Further data on gene amotation and detailed information about changes from previous releases can be found at http://genolist.pasteur.fr/SubtiList/.
Kunst.F., Ogasawara,N., Yoshikawa,H. and Danchin,A.
Direct Submission
Submitted (27-J071-2003) I. Moszer, A. Danchin, Institut Pasteur,
Generique des Genomes Bacteriens, 28 rue du Docteur Roux, 75724
Paris Cedex 15, FRANCE. E-mail: moszer@pasteur.fr,
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Bacillus subtilis complete genome (section 5 of 21): from 813670 to 1011078.

Z99108 AL009126 Z99108.2 GI:32468715

ACCESSION VERSION KEYWORDS

BSUB0005/c DEFINITION

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12378 ATTGCCATCATGAGGGTTTTA---TTGCTGGCCTGCTCATGTATCCGGCTGTTCATCA 12322
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                                                                                                3 (bases 10610 to 12556)
van Sinderen,D., ten Berge,A., Hayema,B.J., Hamoen,L. and Venema,G.
Molecular cloning and sequence of comK, a gene required for genetic
competence in Bacillus subtilis
Mol. Microbiol. 11 (4), 695-703 (1994)
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Haemophilus influenzae (Swiss Prot P44036), Saccharomyces
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Noback,M.A., Terpetra,P., Holsappel,S., Venema,G. and Bron,S.
Direct Submission
Submitted (25-JUN-1997) Noback M. A., University of Groningen,
Dept. of Genetics, Kerklaan 30, Haren, 9751 NN The Netherlands
Location/Qualifiers
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                        J. Bacteriol. 171 (5), 2657-2665 (1989)
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                                                                                        12201 TTCTTGGATGCCGTTCACAATCTCGGCATTACGCCGGGGGGCATCGCAGATGACAACAAA 12142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188 TyriysLysGlulleThrMetAspLysAsnGlnLysValLeuProAlaValAlaAlaLys 207
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Park,S.S., Wong,S.L., Wang,L.F. and Doi,R.H.
Bacillus subtilis subtilisin gene (aprE) is expressed from a sigma A (sigma 43) promoter in vitro and in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA linear BCT 13-OCT-20
region 78-80 degrees: aprE to
                                                    LysAsnargilelleLysProLeuArgAspLysileGlyLysTyrThrServalGlyThr
                                                                                                                                                          108 ArgLysGlnProAsnLeuGluGluIleSerLysLeuLysProAspLeuIleIleAlaAsp
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1 (bases 1 to 104)
Stahl,M.L. and Ferrari,E.
Replacement of the Bacillus subtilis subtilisin structural gene with an In vitro-derived deletion mutation
9. Bacteriol. 158 (2), 411-418 (1984)
                                                                                                                                                                                                                                                                   AsnAsnArgHisLysGlyIleTyrLysAspLeuAsnLysIleAlaProThrIleGluLeu
                                                                                                                                                                                                                                                                                                                                                                       148 LyaserPheAmpGlyAmpTyrAmnGluAmnileAspAlaPheLymThrileSerLymAla
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Bacillus subtilis
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| 11724 TTTACACACGCTGTGAAGTCAGAT-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="WithfrestartsperkalgreseQityhdwdrlsgranwlr
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trapfrwitdbgtpvvlldbymadlsbaadleptidpehppymgftsgstgkkkaf
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89 Asnargileile---LysproLeuArgAspLysileGlyLysTyrThrSerValGlyThr 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68
                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similarity to BioY from Bacillus sphaericus (Swiss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2370 AAGCAGCTGATCAACAAGGATGTGCTGAAGAAATTGACGGCTACACATCTGTCGGCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LysileLeuSerValileGlyLeuLeuPheValLeuIleAlaThrAlaAlaCysGlyAsn
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                                                                                                                                                                                                                                                                                                                           /gene="yhfs"
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Indels:
xref="UniProt/TrEMBL:007619"
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Matches:
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complement(6329. .6336)
                                                                                                                                                                                                                                              complement (4893, .4903)
/gene="yhfS"
                                                                                                                                                                                                                                                                                                 complement (4893. .4903)
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RSRNAHDERFYREEVVALGELETDEAFLKTRPIEAIIPRARVPDTSSGTVTAANSSG
IADGAAALLVMEEEKAAALGIKPVLRFIGSAVSGTHPNFPPAAPVVALRQLLHTHDVT
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RLVNACLSNIERAEEKWRIKDYNINSHLSGFIK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / note= similarity to acetyl-CoAuacetyltransferases (ThiL, encoding the enzyme for the first step in poly-beta-hydroxybutyzate synthesis from Chromatium poly-beta-hydroxybutyzate synthesis from Chromatium vinosum (Swiss Prot P4536), Alcaligenes eutrophus (Swiss Prot P14611), Thiotystis violacea (Swiss Prot P45363), and B.subtilis (Swiss Prot P45855)."
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KAKQLINKDVLKKIDGYTSVGTRSOPEMEKIASLKPDLIIDTTRHKKYNDQLKKIAP

TALANNLANDYQDTIDASLTIAKAVGKEKEMEKKLTAHEEKLSETKQKISANSQSVLL

IGNTNDTIMARDENFFSRLIYQVGYRYAISTSGOSNGGOSVMMMATLEQLLKTD

PDVIILMTGKTDDLDADGKRPIEKNVLMKKLKAVKNGHVYHVDRAVWSLRRSVDGANA
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B.subtilis (EMBL: Z75208), bile acid-CoA ligase from
Bubacterium sp. (Swiss Prot P19409), long-chain-fatty
aciduCoA ligase from E.coli (LcfA; Swiss Prot P29212)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="similarity to a hypothetical protein 0215b from E.coli (Swiss Prot P36942), and to several phosphoglycerate mutase (pgm) proteins, from Treponema pallidum (EMBL: U55214) and Schizosaccharomyces pombe
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                                                                                                                                                                                                                                                                                                                                                                 complement (3136. .3731) /gene="yhfR"
                                                                                                                                                                                                                                                                                                                                                                                                                  complement (3136. .3717)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Swiss Prot P36623).
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/transl_table=11
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TTPSGFDCSGFIXYVLNKVTSVSRLTAAGYWNTWKSVSQPAVGDFVFFSTYKAGPSHV
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On Jul 7, 2003 this sequence version replaced gi:2633260.
This entry contains data from release R16.1 of the SubtiList database. Further data on gene annotation and detailed information about changes from previous releases can be found at http://genolist.pasteur.fr/SubtiList/.
Location/Qualifiers
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Sorokin, A., Tacconi, E., Takadani, H., Takemaru, K.,
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Viari, A., Wamburt, R., Wedler, E., Wedler, H., Weitzenegger, T.,
Winters, P., Wipat, A., Yamamoto, H., Yanama, K., Yasumoto, K.,
Yasuhida, K., Yoshikawa, H.F., Zumstein, E., Yoshikawa, H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (27-JUN-2003) I. Moszer, A. Danchin, Institut Pasteur, Genetique des Genomes Bacteriens, 28 rue du Docteur Roux, 75724 Paris Cedex 15, FRANCE. E-mail: moszer@pasteur.fr, adanchin@pasteur.fr Phone: +33 (0)1 45 68 84 41, Fax: +33 (0)1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Bacillus subtilis subsp. subtilis str. 168"
/mol_type="genomic DNA"
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Nature 390 (6657), 249-256 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 198743)
Kunst, F., Ogasawara, N., Yoshikawa, H. and Danchin, A.
Direct Submission
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function="cell wall lytic activity"
note="alternate gene name: cwlE, yhdD"
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Bacillus subtilis subsp. subtilis str. 168
Bacillus subtilis subsp. subtilis str. 168
Bacillus subtilis subsp. subtilis str. 168
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[Lobes 1 to 199743]
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2787 TACCGATATGCAATCAGT-----ACGTCAGGCAATAGCGATTCAAGCAATGGCGGC 2837
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Bacillus subtilis complete genome (section 6 of 21): from 1011039
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                                                                                                                                                                                                                  188 TyriysiysGluileThrMetAspLysAsnGlnLysValLeuProAlaValAlaAlaLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        228 PheLysGluAlaLeuSerAspAspValThrLysGlyLeuSerLysTyrLeuLysGly---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3078 AAAGAGATGCCGGCTGCTAAGAAATAAAAGAAAAAGACAGGCAAAC 3122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    320 LysGluLeuValGluLeuSerLysLysAspSerLysLysAspAsn 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 ArglysGlnBroAsnLeuGluGluIleSerLysLeuLysProAspLeuIleIleAlaAsp 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 LysileLeuSerValileGlyLeuLeuPheValLeuIleAlaThrAlaAlaCysGlyAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49 GluGlyThrThrLysValProLysHisProLysArgValValValLeuGluTyrSerPhe
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136
70
113
16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                              304 AspLeuTrpAlaArgSerArgGlyLeulleSerSer--------GluGluMetAla
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96944 AAAGAGATGCCGGCTGCTAAGAAATAAAAGAAAGAGGGAAAC 96989
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of AE017333 from base 1100001 (AE017333 Bacillus licheniformis
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|12297 GGAGAAAAAGATAAAGTCGATGAAGACGGAAAAGACCGATCGAAAAAGATCTCTTTGG 12356
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                                                                                                                                                                                                                                                                                               29 AgnSerSerAsnSerSerLysGluSerSerLygAspGlyValGlulleLygHisGlu
                                                                                                                                                                                                                   129 AsnargHisLysGly1leTyrLysAspLeuAsnLysIleAlaProThrIleGluLeuLys
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|12063 AAACAGAAATTCGGC---AGCCGGAAACAGAGCATTCTTCTGCTCGGGAACACAAATGAA
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Matches:
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Pasteurella multocida subsp. multocida str. Pm70 section 14 of 204 of the complete genome.
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                                                                                                                                                             LysglnProAsnLeuGluGluIJeSerLysLeulysProAspLeuIleIJeAlaAspAsn 128
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    AsnSerSerAsnSerSerLysGluSerSerLysAspGlyValGluIleLysHisGlu
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                   ArgSerArgGlyLeuIleSerSerGluGluMetAlaLysGluLeuValGlu---LeuSer
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Matches:
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Pasteurella multocida subsp. multocida str. Pm70 Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Pasteurella. 1 (bases 1 to 13792) May, B.J., Zhang, Q., Li, L.L., Paustian, M.L., Whittam, T.S. and Complete genomic sequence of Pasteurella multocida, Pm70 Proc. Natl. Acad. Sci. U.S.A. 98 (6), 3460-3465 (2001) 21145866 11248100 2 (bases 1 to 13792) Zhang, Q. and Kapur, V. Direct Submission Submitted (24-OCT-2000) Department of Veterinary Pathobiology, University of Minnesota, 1971 Commonwealth ave cr	55108, USA Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Pm70" Amol_type="genomic DNA" Amol_type="genomic DNA" Amol_type="genomic DNA" Amol_type="genomic DNA" Amol_type="gene="molio-"gene-"molio-"gene="molio-"gene="molio-"gene="molio-"gene="molio-"gene-"gene="molio-"gene-"gen	/protein_id="AAKO2200.1" /db_xxef="G1:1272039" /translation="MTFIAYGNIDTYPLDSIPRELLIEKLROPQSSNQRVQKRHRC /translation="MTFIAYGNIDTYPLDSIPRELLIEKLROPQSSNQRVQKRHRC /translation="MTFIAYGNIDTYPLDSIPRELLIEKLROPQSSNQRVQKRHRC RWVAHFILWQLLKISQKPTALLGHIDYSQSGRPQLPVHIDVDFNISHSGDWVAJIRVN TQGDSIVGIDESPQKERDYPALLAYFASPSEQAWFTQQQEKEKSFYLSWCLREAVLK SQGGILVAETTHDAIYYKVNEKT" 994253 /gene="hfix" /note="hfix" /codon start" /codon start=" /transl_table=11	KQNNQBQSPPDIEBIFNNLLKKLGGSGNGGKRNNSHSGGSLNLGKLLPJAAVIGAIW GVSGFYTVKEABERGVNRRFELAIVOPGLHAIVOPGLHAIPWRFFTENDYIPWNEQVKEHTYGSML TQDENMYKVENTWRTLNTIIEPYNMGLEVYDWNFGSARPPEEVKDAFDDAIKAGEDEGRYIR EABAPYRAREREIFRADAORILEEATAYKDRVULDAKGEVERFERLLEFKAAPELLRE RLYIQTMEKWANATRRVMLDGNSGNNLTVLPLEQILKGQQTKGKSTNATSEEVRPVFR 2253. 3140 / gene="hflc" / gene="hflc" / cdon start=1 / transl table=11 / product="hflc" /
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
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Novozymes Biotech, Inc. (US); Novozymes A/S (Di Location/Qualifiers
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12750 GAAGTCCAAGACTTTGTAACGAAATCCGCCAAA 12718
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2 (bases 2) Tanabe, T. and Funahashi, T.

Direct Submission.

Submitted (122-MAR-2002) Shigeo Yamamoto, Okayama University,

Faculty of Pharmaceutical Sciences; 1-1-1 Tsushima-naka, Okayama, Okayama 700-8330, Japan

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Yamamoto, S.
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AB082122 GI:23307109
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480 TCTCAGCTTCTGACGAAAATCGGCTATACATACGTGTCGGAGACAGC---GGCAAAGGC
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Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
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Gaps:
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Hattori,M. Yamashita,A., Oshima,K. and Shiba,T.

Hattori,M. Yamashita,A., Oshima,K. and Shiba,T.

Hattori,M. Yamashita,A., Oshima,K. and Shiba,T.

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This work was done in collaboration with Kozo Makino, Ken Kurokawa, Katsushi Yokoyama, Takayuki Uda, Kenichi Tagomori, Masatomo Najima, Katsushi Yokoyama, Takayuki Uda, Kenichi Tagomori, Masatomo Najima, Rasushi Yokoyama, Takayuki Uda, Kenichi Tagomori, Masatomo Najima, Rasushi Honda, Hideo Shinagawa, Tetsuya lida (Osaka University), Yoshio lijima (Kobe Institute of Health), and supported by the Research for the Future Program of the Japan Society for the Promotion of Science. This clone was isolated from a patient Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nasu,H., Iida,T., Sugahara,T., Yamaichi,Y., Park,K.S., Yokoyama,K., Makino,K., Shinagawa,H. and Honda,T. A filamentous phage associated with recent pandemic Vibrio parahaemolyticus 03:K6 strains J. Clin. Microbiol. 38 (6), 2156-2161 (2000)
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                                                                                                                                                                                                        BCT 07-APR-2004
                                                                                                                                  LysAspprovalTrpLysLysLeuAsnAlaValLysAsnGlnArgValAspIleLeuAsp 302
                                                                                                                                                                                                                                                                                                                                                                            complete sequence, 6/6.
830
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                                                                                      264 MetPhelleMetThrAsnLysAlaSerSerAsnGluProSerLeu---LysGluLeuGlu
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Vibrio parahaemolyticus
Bacteria, Proteobacteria;
Vibrionaceae, Vibrio.
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Mismatches:
Indels:
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Matches:
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492.00
55.11%
34.98%
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Best Local Similarity:
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RILNAIVDTHNAQLTQDPNHETRTMPYSQVLETLHTLTPKGSELILLSDFAHVEEREL
TQLRRLKQHNSVRAIQFYDPLERGETDFRGQAKASDGRRSQWFNFGSTGQRKALETHF
TQHQBSIKQQCHSNAIPFNTLSSGWPLIQQLS"
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EQLEKIYDTINKLEPVSSDTQTWRPQSEWFPYPLSAALVLSMLFLLRRKHG"
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                                                                                                                                                                                                                                                                                                                                                                                    /evidence=not_experimental/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /evidence=not_experimental
                                                                                                            /gene="VPA1453"
/4225. 4771
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5691. .7547
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                                                                                                                                                                                                                               / VGCCE="Gimilar to GB:AAF96089.1 (AE004358) percent
identity 71 in 638 aa"
/ Codon start=1
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/ Codon start=1
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/ Fransl_table=11
/ Fransl_table=11
/ Fransl_table=11
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SERITDISDRNTQVAATATEEQSTVVHTINQNIEEINAINEMTTATAREELAGASRDLQE
COMPLEMENT (2136. . . 2288)
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4184
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nhtsrqkgrgmdfmevrqyqagddirsidwrvtartgkahtklfaedkrgavilytdd
cssehfgsryvlksvqlahfasvliwltlakkdrigaviddgqclefrpsslqkqd
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identity 79 in 318 aa"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="similar to GB:AAF96087.1 (AE004357) percent identity 50 in 309 aa" codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /evidence=not_experimental
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transl table=11
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complement (55, .1971)
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                             db_xref="taxon:670"
chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2287. .3243
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IPSFSADGMKTEPIOLKVTANKSAPDLDDLESFNMSVDNHTLYPQGSANLRMQLIIKA
DTRRLLDNPQVVPPRIEGMKLEPVGEMOQGGRVIGALEVTVENSGFRLITABEQFGFTLL
BOPLTGGST IY GYGGLTGGSTKNEMPISTKVEQMPITVKAIPSEFKGSWLPGSALLOMTGSW
DDQGNTLSARTVNNYKGGSSITRTIÖLKARGTQABYLPRITMDYPNSLRVYPBQPQFD
TARDGTVIMTVKQVLIPTEAGEFTLPGYTLNWWDSKSDEAKQANLSELKLNVEGSBAG
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||| ::: ||||||::: 229243 229446 ACACAAGAAACATTCAGTTTGGTGGTTTCCGACAAAGGGATGTGGTTGCATAGCCCG 229387 229386 GTTTCTTACGCTGGTGGCGTTTTGAGGCACTCTAGGCATCCAAAGCCCGCTGGCTCCATCT 229327 GAG------GAGAATGCGTATATCCCAACCAGCTTTGAACTT 229291 229447 229621 :::::: ||||||| :::::: : ...-AGCGTGCAAGACAAGGCAATTTTGAGCTAGAA 229861 229860 GCGAIACCTCAACGIATIGGGTITITGGAGTITITGTGGACGCTCTGGCGGCGCGTC 229801 229741 255 275 294 AsnGlnArgValAspIleLeuAspArgAspLeuTrpAlaArgSerArgGlyLeuIleSer 314 176 LysargleuGluGluHisaapLysLysIleGluGluTyrLysLysGluIleThrMetAsp 195 LysAsnGlnLysValLeuProAlaValAlaAlaLysSerGlyLeuLeuAlaHisProSer 215 216 AsnSerTyrValGlyGlnPheLeuSerGlnLeuGlyPheLysGluAlaLeuSerAspAsp 235 ileSerLysLeuLysProAspLeuileileAlaAspAsnAsnArgHisLysGlyileTyr 135 LysaspleudsnlysilealaprothrileGluLeuLysSerPheAspGlyAspTyrAsn 155 GluhanIleAspAlaPheLysThrileSerLysAlaLeuGlytysGluGluGluGlyLys 175 ArgAspLysileGlyLysTyrThrServalGlyThrArgLysGlnProAsnLeuGluGlu 115 ASPVALLYSProValGlyIleAlaAspAspAsnLysLysAsnArgIleIleLysProLeu 95 LysGluSerSerLysAspGlyValGluIleLysHisGluGluGlyThrThrLysValPro 55 LeuLeuPheValLeuIleAlaThrAlaAlaCysGlyAsnAsnSerSerAsnSerSer 35 ValThrLysGlyLeuSerLysTyrLeuLysGlyProTyrLeuGlnMetAsnThrGluThr LeuSerGlnValAsnProGluArgMetPheIleMetThrAsnLysAlaSerSerAsnGlu ProSerLeu---LysGluLeuGluLysAspProValTrpLysLysLeuAsnAlaValLys 229800 GATGICICACCGGTAGGCGTIGCCGAIGAGGATGCCAIACGAGTCAICCCTGCTGTI LysHisProLysArgValValValLeuGluTyrSerPheValAspAlaLeuValAlaLeu 335862 110 72 106 23 Length:
Matches:
Conservative:
Mismatches:
Indels: US-10-724-972A-6352 (1-335) x AP005089 (1-335862) 7.81e-25 487.50 58.52% 35.37% 28.85% Percent Similarity: Best Local Similarity: Alignment Scores 196 . 38 276 229326 256 229290 136 96 116 156 26 9/ 16 229956 36 229896 Query Match: DB: .. So Score:

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of BX950851 from base 1100001 (BX950851 Brwinia carotovora subsp
229182 AAACAACAACTGGTCGAAGTCTCTCCGGAACTGTGGTCATTAAATCGCGGCATGTTAGCG 229123
                                                                                     BX950851 Accession BX950851
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Matches:
Conservative:
Mismatches:
Indels:
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GCGGAAGAATTGCCCGCAACCTTGAAGCGTTA 229090
                           SerGluGluMetAlaLysGluLeuValGluLeu 325
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                                                                                                                                       IleIleAlaAspAsnAsnArgHisLysG]yIleTyrLysAspLeuAsnLysIleAlaPro 143
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                                                                                                                                                                         ThrileGluLeuLysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThr 163
                                                                   AspAspAspLysLysAsnArgllelleLysProLeuArgAspLyslleGlyLysTyrThr 103
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
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CTGATTGTGACGCACTATCGC-----GAAGAAGTATTGTGAAACGCTGGCAGCAG
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                                                                                                       ServalGlyThrArgLysGlnProAsnLeuGluGlulleSerLysLeuLysProAspLeu
 44 GlulleLysHisGluGluGlyThrThrLysValProLysHisProLysArgValValVal
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INSECTICIDE PROTEINS FROM PHOTORABDUS LUMINESCENS /i
Patent: WO 03087377-A 1 23-OCT-2003;
INSTITUT PASTEUR (FR); CENTRE NATIONAL DE LA RECHERCHE
ACIBNITIQUE (CINES) (FR); INSTITUT NATIONAL DE LA RECHERCHE
AGRONOMIQUE (INRA) (FR)
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Conservative:
Mismatches:
Indels:
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RHOYDARGYTLHSI DPRIVADAKOADBUSYRPUMOYDLAGHALRTESYDAGRTYALIND
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Direct Submission
Submitsed (13-APR-2003) L. Frangeul, Institut Pasteur, Genopole, 25
Tue du Docteur Roux, 75724 Paris Cedex 15, FRANCE. E-mail:
Location/Qualifiers
1. 349107
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Photorhabdus luminescens subsp. laumondii TTO1 complete genome;
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BX571873.1 GI:3678741

EX571873.1 GI:3678741

Complete genome.

Photorhabdus luminescens subsp. laumondii TTO1

Photorhabdus luminescens subsp. laumondii TTO1

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

Enterobacteriaceae; Photorhabdus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
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TITLE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NTGWKDKAPSGSPEANDAPVAYLTHIYOLALDQEKSGASAIMYTLVERRPDIGALLIN
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142

331262

331202

82

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              331821 AGCAACACCTGGGCTGGTATGGCGGGGTATTGCCGCTGAACGCATTGGCAGTGCG 331880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       331656 -----CATGCGGCAATGTTTCTCTCAACCTGGAACAGTTACTGGCACTCAATCCTGAC 331709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||| ::: ||||||||| :::
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  331443 ATCATCGGCAAAGTCATGGGGAAAGAGAGTGAGAAAGGGCTGGCAGAAGCGCTGGCAGAAGGACGCT 331502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    331557 GGCACCTCGCGCGAACAGCAATTTAACCTGCACCCAGCGATACCTATACCGGCAGCGTC 331616
                                                                                                                                                                                                                                                                                                                                                                                                                                                     |||||||||||||||||::
| CTCATCATTGCAGACAGTCAACGCCACGCGGGATTTATCGGGCACTCAAGGGCATCGCT 331382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   303 ArgAspLeuTrpAlaArgSerArgGlyLeulleSerSerGluGluMetAlaLysGluLeu 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143 ProThrileGluLeuLysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLys 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ThrileSeriysAlaLeuGlyLysGluGluGluGlyLysLysArgLeuGluGluHisAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183 LysLyslleGluGluTyrLysLysGluIleThrMetAspLysAsnGlnLysValLeuPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LeuSerGlnLeuGlyPheLysGluAlaLeuSerAspAspValThrLysGlyLeuSerLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 TyrLeuLysGlyProTyrLeuGlnMetAsnThrGluThrLeuSerGlnValAsnProGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     331503 GAACGCATGAAAGGCTATGCCAGCCAG-----TTGCCACACAGGCGTCAGTGTGTTTTT
                                                                                                                                                                                                                                                                        331203 GCCGATGATAACGATCCGCAGCGATTCTCACCGATGTTCGCCAGCGTATTAAGCCCTGG
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                                                                                                                                                              ValLeuGluTyrSerPheValAspAlaLeuValAlaLeuAspValLysProValGlyile
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                                                                        43 ValGlulleLysHisGluGluGluThrThrLysValProLysHisProLysArgValVal
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6593114.
                                     US-10-724-972A-6352 (1-335) x BX571873 (1-349107)
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AR354237.1 GI:33760321
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331881 GTAAAAATC 331889
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LRVVTPFAITPATPFLDQVFNSVGTFDTPFVIDNQDFVYTLTTGGDGARVKHISTALG
LNHRQFLLLADNIARQGGNITQSTLNCNLFVVSAFYRLANLARTLGTNPESSPCALVDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="unnamed protein product; Similar to pyocin S3
mmunity protein and to Photorhabdus luminescens proteins"
                                                                                                                                                                                                                                                                                                    /notes"unnamed protein product; Similar to pyocin S3
immunity protein and to Photorhabdus luminescens proteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="unnamed protein product; Some similarities with pyocin S3 immunity protein and similar to Photorhabdus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       349107
102
60
107
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CDS

222

242

Unknown Unknown

ORGANISM

Length:
Matches:
Conservative:
Mismatches:
Indels:

5.99e-24 476.00 57.24% 36.04% 28.17%

Percent Similarity: Best Local Similarity:

RBS

Query Match

ORIGIN

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ECOFECECDE 4842 bp DNA linear BCT 26-APR-1993 K-12 fecA gene, 3'end; fecB,C,D,and E genes, complete cds's. M26397 M26397.1 GI:145923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli

Escherichia coli

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

Enterobacteriaceae; Escherichia.

1 (bases 1 to 4842)

Staudenmaier, H., Van Hove, B., Yaraghi, Z. and Braun, V.

Nucleotide sequences of the fecBCDE genes and locations of the

proteins suggest a periplasmic-binding-protein-dependent transport

mechanism for iron(III) dicitrate in Escherichia coli

9.21350
                                                                                                                                                                                                                                          310 ArgGlyLeuileSerSerGluGluMetAlaLysGluLeuValGluLeuSerLysLysAsp 329
                                                                                                                                                                                                                                                                                                                                                                                                         302 CGTGGCTTAATTTCTTCTGAAGAAATGGCTAAAGAACTTGTTGAATTATCAAAAAAGAA 361
                                                                                                             210 LeuLeuAlaHisProSerAsnSerTyrValGlyGlnPheLeuSerGlnLeuGlyPheLys
                                                                                                                                2 TIATTAGGACATCCAAACTATTCATATGTTGGACAATTTTTAAACGAACTAGGATTTAAA
                                                                                                                                                                                                                           GlnMetAsnThrGluThrLeuSerGlnValAsnProGluArgMetPheIleMetThrAsn
                                                                                                                                                                                                                                                                               270 LysAląSerSerAsnGluProSerLeuLysGluLeuGluLysAspProValTrpLysLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source text: Escherichia coli (strain K-12)
Location/Qualifiers
            91
15
0
0
        Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                      US-10-724-972A-6352 (1-335) x AR535793 (1-668)
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    4842
    organism="Escherichia

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[. . .136
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/gene="fecA"
       475.00
86.89%
74.59%
28.11%
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                  Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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TITLE
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Mansch,C.A., Choi,G.A., Barash,S.C., Dillon,P.J., Fannon,M.R. and
            1 (bases 1 to 668)

Kunsch,C.A., Choi,G.H., Barash,S., Dillon,P.J., Fannon,M.R. and Rosen,C.A.

Staphylococcus aureus polynucleotides and sequences

Patent: US 6593114-A 355 15-JUL-2003;

Location/Qualifiers
                                                                                                                                                                                                                                                                                                210 LeuLeuAlaHisProSerAsnSerTyrValQlyGlnPheLeuSerGlnLeuGlyPheLys
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Location/Qualifiers
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AF326777 66714 bp DNA linear BCT 18-JUN-2002
Shigella flexneri 2a SRL pathogenicity island, complete sequence.
AF326777
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Shigella flexneri 2a
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CP4-57 of Escherichia coli K-12"
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Luck,S.N., Turner,S.A. and Rajakumar,K.
Direct Submission
Submitted (06-DEC-2000) Microbiology, Monash University, VIC 3800,
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4 (bases 1 to 66714)
Luck,S.N., Turner,S.A. and Rajakumar,K.
Direct Submission
Submitted (18-JUN-2002) Microbiology, Monash University, VIC 3800,
                                                                                                                                                                                                                                         3 (Dases 1 to bb/14)
Luck,S.N., Turner,S.A. and Rajakumar,K.
Direct Submission
Submitted (17-MAY-2002) Microbiology, Monash University, VIC 3800,
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CP4-57 of Escherichia coli K-12"
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8, 2002 this sequence version replaced gi:15808696.
Location/Qualifiers
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619. .1836
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K,S.N., Turner,S.A. and Rajakumar,K.
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On Jun 18,
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                                                                                                                                                                                                                                                                                                                      TITLE
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AUTHORS
TITLE
JOURNAL
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38705 gcaddircarccaraccarccarcaccaradacaachacaacadacaardchaardchacarada 38646
                                                                                                                                                                                                                                                                                                                                38795 TCACGCGAACAGCAATTCAACCTGCATACTCAGGAGCCTGGACCGGGCGCGTGCTGGCC 38736
38909 GGCGAAATGGTGGGTAAAAGCGAGAGATGCAGGCACGTCTGGAACAACATAAAGAGG 38850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAT 16-FEB-2002
                                                                                                                                                                      244
                                                                                                                                                                                                                                                                                                                                                                        AsperovaltrpLysLysLeuAsnalavalLysAsnGlnArgvalAsplleLeuAspArg 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84
                                                                                                                                                                                                                                     245 LysGlyProTyrLeu---GlnMetAsnThrGluThrLeuSerGlnValAsnProGluArg 263
                               185 IleGluGluTyrLysLysGluIleThrMetAspLysAsnGlnLysValLeuProAlaVal 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45 IleLysHisGluGluGlyThrThrLysValProLysHisProLysArgValValValLeu
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                                                                                                                                                                                                                                                                                                       MetPhelleMetThrAsnLysAlaSerSerAsnGluProSerLeuLysGluLeuGluLys
                                                                                                                                                                                                                                                                                                                                                                                                                                         304 AspLeuTrpAlaArgSerArgGlyLeulleSerSerGluGluMetAlaLysGluLeuVal
                                                           ::: ::::!!|
38849 ATGGCGAGGCAGCCAGCCAG-----CTTCCCAAAGGGACACGCGTGGCCTTTGGCACA
                                                                                                   205 AlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPheLeuSer
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100
62
104
16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
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Sequence 14 from Patent WO0170776.
AX370197
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57.45%
35.46%
27.22%
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Best Local Similarity:
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VLFGTCALLYSQGATTPLIIPLAVALDVPTWAILASYVAVTGVFVLPTYFTSLAAMEF
DTTGTTRVGKYVLNHPPMLPGLGGIIAGVALGFVIAPMII"
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                                                                                                                                                                                                                                                                                                                                                                                                      /notes"confers streptomycin and spectinomycin resistance;
similar to AadAl from Tn21 on plasmid R100"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64
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              to DcuA in Escherichia coli K-12"
                                                                                                                                                                                                                                                   complement(<14553. .>15322)
/note="remnant of IS600-like element; central region
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/note="IS1 element"
complement(16171. .16962)
/qene=">aaAa1
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                   note="Orf9; similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                              table=11
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/transl_table=1
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U00096_16

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U00096_19

U00096_22

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U00096_25

U00096_25

U00096_26

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7375 GGCGAAATGGTGGGTAAAAGCGAGAGATGCAGGCACGTCTGGAACAACATAAAGAGAGG 7316
7675 GAACTCTCGTTCGCCGATGCGCTGGCCGTGGACGTCATCCCGATCGGTATTGCCGAC 7616
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7315 ATGCCGAGTGGGCCAGCCAG-----CTTCCCAAAGGACACGCGTGGCCTTTGGCACA 7262
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|7615 GATAACGATGCAAAACGCATCCTGCCCGAAGTGCGTGCGCACCTGAAACCGTGGCAGTCC
                          AspAsnLysLysAsnArgllelleLysProLeuArgAspLyslleGlyLysTyrThrSer
                                                                                              205 AlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPheLeuSer
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||||||| |12142 GATAACGATGCAAAGCATCCTGCCCGAAGTGCGTGGGCACCTGAAACCGTGGCAGTCC 12083 GECGAAATGGTGGGTAAAAGCGAGAGATGCAGGCACGTCTGGAACAACAACAAAGAGAGG 11843 85 AspAsnLysLysAsnArgileIleLysProLeuArgAspLysIleGlyLysTyrThrSer 104 165 SerLyaAlaLeuGlyLysGluGluGluGlyLysLysArgLeuGluGluHisAspLysLys 184 45 IleLysHisGluGluGlyThrThrLysValProLysHisProLysArgValValValLeu 125 IleAlaAspAsnAsnAsnAsgHisLysClylleTyrLysAspLeuAsnLysIleAlaProThr 145 IleGluĻeuĻysSerPheAspGlyAspTyrAsnGļuAsnIleAspAlaPheLysThriļe 11902 g ઠે a 8 ð 셤 ठ g 장수염

LOCUS U00096 Accession U00096

fragments

Sequence split into 47

110000 210000 310000 510000 610000 710000 11110000 1310000 1310000

100001 200001 400001 500001 700001 900001 1000001 1100001 1300001

Fragment Name 100095 00 100095 00 100095 01 100095 03 100095 04 100095 05 10 100095 10 100095 11 100095 12 100095 13

Length:
Matches:
Conservative:
Mismatches:
Indels:

2.39e-23 460.00 57.45% 35.46% 27.22%

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/map="92.8 to 100 minutes"
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Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes.
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This sequence was determined as part of the E. coli Genome Project (Frederick R. Blattener, director) at the University of Misconsin-Madison. Supported by award HG00301 from the NIH Human Genome Project. The entire sequence was independently determined from E. coli MG1655; overlaps with other sequence determined are annotated. The start of this entry overlaps the end of the entry ECUWW89 (100006) by 1885 bp.
                                                                                                                                                                                                                                                                                   245 LysGlyProTyrLeu---GlnMetAsnThrGluThrLeuSerGlnValAsnProGluArg 263
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                                                                                                205 AlaalaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPheLeuSer 224
    IleGluGluTyrLysLysGluIleThrMetAspLysAsnGlnLysValLeuProAlaVal 204
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Enterobacteriaceae, Escherichia.
1 (bases 1 to 338534)
Burland, V., Plunkett, G. III, Sofia, H.J., Daniels, D.L. and
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Direct Submission
Submitted (12-AUG-1994) Guy Plunkett III, Laboratory of Genetics,
University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
Email: ecol@genetics.wisc.edu Phone: 608-262-2534 Fax:
608-263-7459
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Nucleic Acids Res. 23 (12), 2105-2119 (1995)
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/strain="K-12"
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/db_xref="taxon:562"
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/mcre="This sequence comprises the following lambda clones: DD928(EC27-278), DD930(EC30-188), EC27-1070), DD931(EC27-188), EC27-1070), DD931(EC27-1070), DD931(EC27-1070), DD941(EC17-142), DD945(EC17-8), DD947(EC244-34), DD949(EC22-169), DD952(EC17-103), DD952(EC17-104), DD952(EC27-104), DD956(EC30M-1), DD966(EC30M-1), DD970(EC19-202), DD974(EC19-61), DD976(EC18-233), DD977(EC30-M-1), DD997(EC18-115), DD997(EC18-13), DD997(EC17-116), DD997(EC17-116), DD997(EC17-116), DD997(EC18-113); M13mp19 or Janus vectors were used for subcloning"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GIEDBAKTLGVSVDI FASPESEDFOGOLOLFEDLSNRNYKGIAFAPLSSVNLVMPVAR
AWKKGI YLVNLDEKI DMDNLKKAGGNVEAFVTTDNVAVGAKGAFI I DKLGAEGGBEVA
I I CGARGARSGBRARGATERFKKAGSOTKLVASOPADWDR I KALDVATNVLGRNPNI K
AI YCANDTMAMGVAQAVANAGKTGKVLVVGTDGI PEARKMVEAGQMTATVAQNPADIG
ATGLKLMVDAEKSGKVI PLDKAPEFKLVDSI LVTQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein id=nAAA96987.1"
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BYFLTTNNITQIFVQSSVTVLIGMGEFFAILVAGIDLSVGAILALSGMVTAKLMLAGV
DPFLAAMIGGVLVGGALGAINGCLVNWTGL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard_name="REP; repetitive extragenic palindromic

    1. 1885
/note="1885 bp overlap with end of GenBank Accession
Number U00006 (ECOWU89)"

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/note="ORF_f326 of GenBank Accession Number U00006
(ECOWU89)"
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/note="predicted bend of 73.22 degrees"
complement(3030. .3953)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="predicted bend of 75.10 degrees"
complement(377, .1909)
/note="ORF_f510"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         309. .931
/note="predicted bend of 74.75 degrees"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="contains 1 REP sequence" complement (2036. .2971)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1768. .1889
/note="predicted bend of 75.87
complement(1983. .2010)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
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/db_xref="G1:1263173"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              flh-regulated promoter" complement (1985. .2021)
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/label=ORF_f311
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/label=ORF f510
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205073 GITCAGGACGAACACGCACGTTACACTCGAAAAACGCCACAACGGATTGTGGTGCTG 205014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204773 CIGCTGCTTAAGTCCCGCAACGAAACTTAGGAAATTTGCAATCTGGGGCTATCATC 204714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           204713 GGCGAAATGGTGGGTAAAAAGCGAGAGATGCAGGTCTGGAACACATAAAGAGAGG 204654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204599 TCACGCGAACAACTTCAACCTGCATACTCAGGAGACCTGGACCGGCAGCGTGCTGGCC 204540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /trānslation="MMGKLIMLMGPSGSGKDSLLAELRLREGTQLLVAHRYITRDASA
GSENHIALSEQEFFTRAGQNLLALSWHANGLYYGVGVEIDLWIHAGFDVLVNGSRAHL
PQARARYQSALLPVCLQVSPEILRQRLENRGRENASEINARLARAARYTPQDCHTLNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  204449 CIGCIGGTTGCCCACTATCGC-----GAAGAGACATTGTTAAACGCTGGCAACAA 204399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 IleAlaAspAsnAsnArgHisLysGlylleTyrLysAspLeuAsnLyslleAlaProThr 144
                                    nucleotide binding protein (ATP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 IleGluLeuLysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThrIle 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  165 SerLysAlaLeuGlyLysGluGluGluGlyLysLysLysLysLysLysLysLys 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 IleGluGluTyrLysLysGluIleThrMetAspLysAsnGlnLysValLeuProAlaVal 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85 AspAsnLysLysAsnArgileIleLysProLeuArgAspLysIleGlyLysTyrThrSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||||||
204953 GATAACGATGCAAAAGCATCCTGCCGAAGTGCGTGCGCACCTGAAACCGTGGCAGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105 ValglyThrArgLysGlnProAsnLeuGluGluIleSerLysLeuLysProAspLeuIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204833 ATTGCCGACAGCGAGTCGCCATGCGGGGTTTACATCGCCTTGCAGCAAATCGCGCGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45 IleLysHisGluGluGlyThrThrLysValProLysHisProLysArgValValValLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 GluTyrSerPheValAspAlaLeuValAlaLeuAspValLysProValGlyIleAlaAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  205 AlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPheLeuSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlnLeuGlyPheLysGluAlaLeuSerAspAspValThrLysGlyLeuSerLysTyrLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204539 TCTCTGGGGCTG----------AACGTTCCCGCTGCGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    245 LysGlyProTyrLeu---GlnMetAsnThrGluThrLeuSerGlnValAsnProGluArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MetPhelleMetThrAsnLysAlaSerSerAsnGluProSerLeuLysGluLeuGluLys
                                                                                                                                                                                                                                                                                                                                                   338534
100
62
104
16
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
                                                                                                                                                                                                                   DGSLROSVOTLLTLIHQKEKHHACL"
complement (7010. .8146)
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complement (7010. .8146)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (1-338534)
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/db_xref="GI:536938"
.7010)
                 /gene="phnN"
/note="HisP-like
complement (6453.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-724-972A-6352 (1-335) x ECOUW93
                                                                                                                                                                                                                                                                                                                                               9.21e-23
460.00
57.45%
35.46%
27.22%
                                                         protein) "
                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                            Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match:
                                                                                                                                                                                                                                                                                                                                               Pred. No.:
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/bc xref="G1:53633"

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IVEWLIARGALION-BALIDDYBLALAVGEDAMIVKVSKLIGFSGFRNLRSALEDYFSQSE

GVLPSELAFDBARDDVNNKVFNITLRTIMEGQSIVNVDEIHRAARFFYGARQRDLYGA

GGSNAICADVOUKKELRICYRCGAYPDHIMMNSASLLQEGDVVLVVTHSGRTSDVKAA

VELAKKGGAKIICTHSCYASPIAKLADYIICSPAPETPLLGRNASARILQLTLLDAFF

complement (3952. 3979)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAA96989.1"
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HYASQVALAVAGGEVDGGILIGGTGVGISIAANKFAGIRAVVCSEPYSAQLSRQHNDT
NVLAFOSRVGLELEARNIVDAMLGAQYEGGRHQQRVEAITAIEQRRN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (4520. .16191)
/note="corresponds to GenBank Accession Number D90227
(ECOPHN) 1. 11672; the related sequence GenBank Accession
Number J05260 (ECOPHNAQ) is from E. coli B, not K-12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KFNDATTLIDAGLHDLADRWSFGSFQOFLLTHYHMDHVQGLFPLRWGVGDPIPVYGPP
DEQGCDDLFKHPGLLDFSHTVEPFVVFDLQGLQVTPLPLNHSKLTFGYLLETAHSRVA
WLSDTAGLPEKTLKFLRNNQFQVMVMDCSHPPRADAPRNHCDLNTVLALNQVIRSPRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation="MSLTLTLTGTGGAQGVPAWGCECAACARARRSPQYRRQPCSGVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="mpacelrpatgydtdavyalicelkgabedhhafrugenanlrd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="phnQ"

/note="annotated in GenBank Accession Number J05260

(ECOPHNAQ), but probably not a gene"

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ISM Pseudomonas syringae pv. tomato str. DC3000

Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,

Bacteria, Proteobacteria, Gammaproteobacteria,

Bacteria, Proteobacteria, Gammaproteobacteria,

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Bacteria, Pseudomonas.

Estadomonadaceae, Pseudomonas.

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The complete genome sequence of the Arabidopsis and tomato pathogen

Proc. Natl. Acad. Sci. U.S.A. 100 (18), 10181-10186 (2003)
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                                                                                                                                                                                    323
                                                                                                                                                                            AspleuTrpAlaArgSerArgGlyLeulleSerSerGluGluMetAlaLysGluLeuVal
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AE016858 AE016853
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KEYWORDS
SOURCE
ORGANISM
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AE016858/c
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DEFINITION
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gene		Aspīle

Length: Matches:

Alignment Scores: Pred. No.: Score:

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------CAG 164349
                                                                                                                 |LysGlnProAsnLeuGluGluIleSerLysLeu 119
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:TGGCAACCCAATATCGAAGTGATCGCACGGCTC 164109
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|TCACGCGGCGAGGACTATCAGGGCAGCCTGAAA 163989
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|GGCAAAGGCCCGGAGATGCAGGCGCGAATCGCA 163929
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  GluTyrSerPheValAspAlaLeuValAlaLeuAspValLysProValGlyIleAlaAsp
                                          85 AspAsnLysLysAsnArglleIleLysProLeuArgAspLysIleGlyLysTyrThrSer
                                                     15946 TCCTGGACAGGGATCCTTGGTATAAGGATATTCAAGCGATATGAAAGGGTTAAGCAA
                                                                                                                           IleAlaAspAsnAsnArgHisLysGlyileTyrLysAspLeuAsnLysIleAlaProThr
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                15886 ACAAATGAAGGAACCGAAGGCCTTTTGGAACTCGGAATCAAACCTGTGGGTGCAGTCAAA
                                                                                  ValGlyThrArgLysGlnProAsnLeuGluGluIleSerLysLeuLysProAspLeuIle
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Act 74986 Staphyloc
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Aas51821 Staphyloc
Abt15015 Pathogen
Aca20079 Prokaryot
Act 74415 Staphyloc
Act 74415 Staphyloc
Act 8534 Staphyloc
Act 83786 DNA encod
Adf 30765 Bacillus
Aca4237 Prokaryot
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AAS46238
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98US-00134001.
99US-00450969.
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71.8 1044
69.9 927
43.0 960
42.9 957
42.9 960
42.9 975
42.9 2247
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40.2 5718
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29-NOV-1999;
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(BUSH/)
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Aca47084 Prokaryot
Aas54519 Staphyloc
Acc48532 Staphyloc
Aca19774 Prokaryot
                                                                                                                 November 9, 2005, 10:23:21; Search time 641 Seconds (without alignments) 3093.781 Million cell updates/sec
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1690
1 GVESVRGLKILSVIGLLFVL......EEMAKELVELSKKDSKKDNK 335
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             GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                4390206 seqs, 2959870667 residues
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Searched:

0.5 7.0

BLOSUM62 Xgapop 10.0, Xgapext Ygapop 10.0, Ygapext Fgapop 6.0, Fgapext Delop 6.0, Delext

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

SUMMARIES

Query Match Length DB

Score 1690 1671 1242 1233 1232

So. Result

genesegn2003ds:* genesegn2004as;* genesegn2004bs:*

geneseqn2003cs: genesegn2002bs:*genesegn2003as:*genesegn2003bs:*

geneseqn2000s;* geneseqn2001as;* geneseqn2001bs;* geneseqn2002as;*

geneseqn1980s:* geneseqn1990s:* Geneseq_16Dec04:*

Database :

ADS03285 ACA47084 AASS4519 ACC48532 ACA19774

1008 993 1014 2981 984

100.0 98.9 73.5 73.0

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261 ProGluargMetPhelleMetThrAsnLysAlaSerSerAsnGluProSerLeuLysGlu 280
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                                                                                                                                                                                             The invention describes an isolated nucleic acid comprising a nucleotide sequence with any of 3772 fully defined nucleotide sequences (SEQ ID NO: 1-3772) and encoding an Staphylococcus epidemidis polypeptide with any cc of 3772 fully defined amino acid sequences (SEQ ID NO: 3772-7544) as given in the specification. Also described are: a recombinant expression vector of (1); vector; a cell comprising a recombinant expression vector of (1); comprising a nucleotide sequence of at least 8 nucleotides in length; a comprising a nucleotide sequence of at least 8 nucleotides in length; a vaccine composition for prevention or treatment of an S. epidermidis of the composition for prevention or treatment of an S. epidermidis of a subject for S. epidermidis infection; compastion of an S. epidermidis polypeptide or its fragment; a subject for S. epidermidis polypeptide or its fragment; a subject for S. epidermidis polypeptide or its fragment; a computer readable medium having recorded in it the nucleotide sample; a computer readable medium having recorded in it the nucleotide sample; a computer readable medium having recorded in it the nucleotide system for identifying fragments of the Staphylococcus genome of commercially importance; a computer based system for identifying fragments of the Staphylococcus genome and/or plasmids; and identifying an expression modulating fragment of the Staphylococcus some and/or plasmids; and identifying an expression modulating fragment of the Staphylococcus some and/or plasmids; and identifying an expression modulating fragment of the Staphylococcus genome and/or plasmids; and identifying an expression modulating fragment of the Staphylococcus some and/or plasmids; and identifying an expression modulating fragment of the present invention are useful for the diagnosis, prevention and/or treatment of an Staphylococcus endodes a S. epidermidis protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polypeptide and encoding nucleic acid derived from Staphylococcus epidermidis, useful for diagnosing, preventing and/or treating an S. epidermidis bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1008 BP; 404 A; 129 C; 188 G; 287 T; 0 U; 0 Other;
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                                                                                                                                                                       Claim 5; SEQ ID NO 2580; 741pp; English.
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Best Local Similarity:
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DB:
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GlnPheLeuSerGlnLeuGlyPheLygGluAlaLeuSerAspAspValThrLygGlyLeu

SeriysTyrLeulysGlyProTyrLeuGlnMetAsnThrGluThrLeuSerGlnValAsn

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LeuproalavalalaalaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGly

HisAspLysLysLysIleGluGluTyrLysLysGluIleThrMetAspLysAsnGlnLysVal

200 9 220

PhelygThrIleSerLygAlaLeuGlyLygGluGluGluGlyGlyRygLygArgLeuGluGlu

160 480 180 540 LeuGluLysAspProValTrpLysLeuAsnAlaValLysAsnGlnArgValAspIle 300

LeuaspargaspLeuTrpAlaargSerargGlyLeulleSerSerGluGluMetAlaLys

GlubeuvalGlubeuSerLysLysAspSerLysLysAspAspLys 335

196

321

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Antisense; ds; prokaryotic essential gene; cell proliferation; drug design; gene.
                                                                          Prokaryotic essential gene #28741.
                                                                                                                                                                                                     21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-0CT-2001; 2001US-0034923P.
08-FEB-2002; 2002US-00362891.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                     21-MAR-2002; 2002WO-US009107
                  ACA47084 standard; DNA; 993
                                                                                                                           Staphylococcus epidermidis
                                                                                                                                                                                                                                                                  (ELIT-) ELITRA PHARM
                                                                                                                                                WO200277183-A2.
                                                        19-JUN-2003
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                                      ACA47084;
LyaTyrThrSerValGlyThrArgLysGlnProAsnLeuGluGluileSerLysLeuLys 120
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                                                                                                                                          ValValValLeuGluTyrSerPheValAspAlaLeuValAlaLeuAspValLysProVal
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Zyskind JW; Xu HH; Ohlsen KL, Forsyth RA, Haselbeck R, Yamamoto R, Malone C, Carr GJ, Zamudio C, Trawick JD, ָה נָי

2003-029926/02 P-PSDB; ABU43214 New antisense nucleic acids, useful for identifying proteins or scre for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

SEQ ID NO 34954; 1766pp; English. Claim

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

CC (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid, (2) an bost cell containing the vector; (3) an isolated on the polypeptide (4) an antibody capable of specifically binding the polypeptide (5) producing the polypeptide; (6) inhibiting cellular comply perpende (5) producing the polypeptide; (6) inhibiting cellular comply sense nucleic acid; (4) an antibody capable of specifically binding the polypeptide (5) producing the polypeptide; (6) inhibiting cellular comply sense product or that has an activity against a biological pathway in which a proliferation, or that has an activity against a biological pathway of the proliferation, or that that inhibits cellular proliferation of an agene required for cellular proliferation or the biological pathway in which a proliferation-required gene or the biological pathway in which a proliferation or multiple cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound is activity; (11) a culture comprising strains in which the test compound that inhibits proliferation of an organism. The antisense nucleic acids required for proliferation of an organism. The antisense nucleic acids required for cellular proliferation in cells other than S. aureus, S. typhimurium, continued for proliferation in cells other than S. aureus, S. typhimurium, a proventy and discovery programs, or for screening for homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, be neutronic format directly from WiPon at sevent or the printed specification, but was obtained in cell certuring the sequence and a compound and organism. The present sequence are one of the target for no int form part of the p ftp.wipo.int/pub/published_pct_sequences

U; 0 Other; Sequence 993 BP; 398 A; 128 C; 183 G; 284 T; 0

993 331 0 0 0 Length:
Matches:
Conservative:
Mismatches: Gaps: 3.44e-152 1671.00 100.00% 100.00% 98.88% Score: Percent Similarity: Best Local Similarity: gnment Scores: Query Match: DB:

US-10-724-972A-6352 (1-335) x ACA47084 (1-993)

8

GTGAGAGGITTAAAAATTITAAGTGTAATTGGCTTATTGTTTGTTTTAATTGCAACTGCA 60 24 44 ValArgGlyLeuLysIleLeuSerValIleGlyLeuLeuPheValLeuIleAlaThrAla AlaCysGlyAsnAsnSerSerAsnSerSerLysGluSerSerLysAspGlyValGlu 25 61 g ò 셤

IleLysHisGluGluGlyThrThrLysValProLysHisProLysArgValValValLeu 45 121

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GluTyrSerPhevalAspAlaLeuValAlaLeuAspValLysProValGlylleAlaAsp 65 181

AspAsnLysLysAsnArgllelleLysProLeuArgAspLysIleGlyLysTyrThrSer 104 85

124 144 480 SerLysAlaLeuGlyLysGluGluGluGlyLysLysArgLeuGluGluHisAspLysLys 184 204 600 224 244 720 264 780 284 840 304 LeuTrpAlaArgSerArgGlyLeuIleSerSerGluGluMetAlaLysGluLeuValGlu 324 ValGlyThrArgLysGlnProAsnLeuGluGluIleSerLysLeuLysProAspLeuIle GTAGGAACACGTAAGCAACCTAACTTAGAAGAAATCAGTAAACTTAAAACTTTAATT ATTGAACTGAAAAGTTTCGATGGAGATTATAATGAAAATATTGATGCTTTTAAAACAATT AlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPheLeuSer GlnLeuGlyPheLysGluAlaLeuSerAspAspValThrLysGlyLeuSerLysTyrLeu ProValTrplysLysLeuAsnAlaValLysAsnGlnArgValAspIleLeuAspArgAsp LysGlyProTyrLeuGlnMetAsnThrGluThrLeuSerGlnValAsnProGluArgMet PhelleMetThrAsnLysAlaSerSerAsnGluProSerLeuLysGluLeuGluLysAsp LeuSerLysLysAspSerLysLysBaspAspLys 335 541 105 301 125 145 421 165 185 481 205 225 245 781 661 265 285 841 901 305 325 961 RESULT 3 8 g ò g 셤 ò ઠે g ò g ò g g ઠે g ò ò ద ò g ò 셤 ઠ d

AAS54519 standard; DNA; 1014

AAS54519;

13-FEB-2002

(first entry)

cellular proliferation gene; antibiotic; Staphylococcus aureus DNA for cellular proliferation protein #831. Antisense; ds; prokaryotic antibacterial; drug design.

Staphylococcus aureus.

64

WO200170955-A2.

27-SEP-2001

84

21-MAR-2001; 2001WO-US009180

21-MAR-2000; 2000US-0191078P

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AATTATACTTCTGTAGGTACACGTAAACAGCCAAACTTAGAGGAAATTAGTAAATTAAAA 378
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TTACAAGAAGATCCAACTTGGAAAAGTTGAACGCAGTTAAAATAATCGCGTGGATATT
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                                      ProAspLeullelleAlaAspAsnAsnArgHisLysGlylleTyrLysAspLeuAsnLys
                                                                                                                141 IlealaProThrIleGluLeuLysSerPheAspGlyAspTyrAsnGluAsnIleAspAla
                                                                                                                                                                                          PhelysThrileSerlysAlaLeuGlyLysGluGluGluGlyLysLysArgLeuGluGlu
                                                                                                                                                                                                                                                                                               LeuProAlaValAlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGly
                                                          HisAsplysLysIleGluGluTyrLysLysGluIleThrMetAspLysAsnGlnLysVal
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                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes their use in the discovery of novel antibiotics, the essential genes coli, Staphylococcus aureus, Salmonalla typhi, Klebsiella pheumoniae, coli, Staphylococcus aureus, Salmonalla typhi, Klebsiella pheumoniae, con setul for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to dentify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins continued compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous uncleic acids which are required for cell proliferation in a wide variety of of organiems. The present sequence encodes an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent continued for the printed specification, but was obtained in the first and the continued in the continued in the continued in the continued in the continued in the continued in the continued in the continued in the continued in the continued in the continued in the continued in the continued in the continued in the continued in the continued in the continued in the continued in the continued in the continued in the continued in the continued in the continued in the continued in the continued in the continued in the continued in the continued in the continued in the continued in the continued in the continued in the continued in the continued in the continued in the continued in the continued in the continued in the continued in the continued in the continued in the continued in the continued in the continued in the continued in the continued in the continued in the continued in the continued in the continued in the continued in the continued in the continued in the continued i
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                                                                                                                                                                                          Trawick JD,
                                                                                                                                                                                                                                                                                                         New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids.
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                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 8156; 511pp; English.
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                                                                                                                                                                                          Zyskind JW,
            23-MAY-2000; 2000US-0206848P.
26-MAY-2000; 2000US-0207727P.
23-OCT-2000; 2000US-0242578P.
27-NOV-2000; 2000US-0253625P.
22-DEC-2000; 2000US-0257361P.
16-FEB-2001; 2001US-0269308P.
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Yamamoto RT, Xu HH;
                                                                                                                                                        (ELIT-) ELITRA PHARM INC
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(DSQU-) D-SQUARED BIOTECHNOLOGIES WPI; 2003-300870/29 P-PSDB; ABR41865. Scott DL; Novel

Novel surface-exposed immunogenic polypeptide of Staphylococcus aureus containing receptors for siderophores or iron-binding ligands, useful for producing antibodies effective against Staphylococci infection. surface-exposed immunogenic

Claim 4; Page 53; 62pp; English.

The present sequence is that of DNA encoding novel Staphylococcus aureus surface-exposed immunogenic polypeptide (SEIP) D2 SA03. To isolate SEIP auriaces, an expression library of S. aureus genomic DNA was screened with anti-SEIP antisera. DNA was isolated from clones expressing SEIPs, and functional domains. The SEIP encoded by the present DNA sequence has sequence homology with the siderophore family of periplasmic binding production and recovery of SEIPs. The SEIPs can be used individually, or in combination, to produce anti-staphylococcal antibodies useful in passive or active immunisation strategies to prevent or contain straphylococcal infection. They can also be used to develop diagnostic авваув

T; 0 U; 0 Other; C; 386 G; 1048 Sequence 2981 BP; 988 A; 559

2981 238 42 51 1 Length: Matches: Conservative: Mismatches: Indels: Gaps: 3.36e-109 1233.00 84.59% 71.90% Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores:

US-10-724-972A-6352 (1-335) x ACC48532 (1-2981)

1814 1634 100 140 120 | IleAlaProThrIleGluLeuLysSerPheAspGlyAspTyrAsnGluAsnIleAspAla 160 20 40 9 80 GlyValGluSerValArgGlyLeuLysIleLeuSerValIleGlyLeuLeuPheValLeu LysTyrThrSerValGlyThrArgLysGlnProAsnLeuGluGluIleSerLysLeuLys 1573 ATTGCACCACACATTATCATTAAAGAGTTTTGATGGAGACTACAAAAAAATATTAATTCG AspGlyValGlulleLysHisGluGluGlyThrThrLysValProLysHisProLysArg 61 ValvalvalLeuGluTyrSerPheValAspAlaLeuValAlaLeuAspValLysProVal GlyileAlaAspAspAsnLysLysAsnArglielleLysProLeuArgAspLyslleGly ProAspleuileilealaAspAsnAsnArgHislysGlyIleTyrLysAspleuAsnLys н 101 41 1753 1633 81 121 141 ઠે 셤 ઠે g ò 셤 ઠે g ò g 요 셤 ઠે ઠે ò

screening

PheLysThr11eSerLysAlaLeuGlyLysGluGluGluGlyLysLysArgLeuGluGlu 180

161

1454 1394 1334 1274 1214 240 |||::::::||| |TACAAGAAGATGCAACATGGAAAAGTTGAATGCAGTTAAAAATAATCGCGTGGATATT 1094 200 GlnPheLeuSerGlnLeuGlyPheLysGluAlaLeuSerAspAspValThrLysGlyLeu HisAspLysLysIleGluGluTyrLysLysGluIleThrMetAspLysAsnGlnLysVal LeuProAlaValAlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGly ProGluArgMetPhelleMetThrAsnLysAlaSerSerAsnGluProSerLeuLysGlu LeuGluLysAspProValTrpLysLysLeuAsnAlaValLysAsnGlnArgValAspIle LeuAspArgAspLeuTrpAlaArgSerArgGlyLeuIleSerSerGluGluMetAlaLys Zyskind JW; Xu HH; New antisense nucleic acids, useful for identifying proteins or scre for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs. ds; prokaryotic essential gene; cell proliferation; ¥Š. Ohlsen Porsyth Haselbeck R, Yamamoto R, Malone C, Carr GJ, 21-MAR-2001; 2001US-00815242. 06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0342923P. 08-FEB-2002; 2002US-00072851. 21-MAR-2002; 2002WO-US009107 08-FEB-2002; 2002US-00072851 06-MAR-2002; 2002US-0362699P 984 gene (first entry) (ELIT-) ELITRA PHARM INC. DNA; Staphylococcus aureus Zamudio C, Trawick JD, WPI; 2003-029926/02. P-PSDB; ABU15904. ACA19774 standard; drug design; gene. WO200277183-A2 19-JUN-2003 Prokaryotic 03-OCT-2002 Antisense; 1453 1393 1333 1273 261 1213 1153 301 221 241 181 201 281 ACA19774; ņ, Wang Wall RESULT 5 8 셤 ò g ò g ò g g g ð ò ઠે 셤 g ò

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The invention relates to an instrated nutritication where expression of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

Co fithe nucleic acid inhibits proliferation of a cell. Also included are:

Co encoding a polypeptide whose expression is inhibited by the antisense

nucleic acid; (2) a host cell containing the vector; (3) an isolated

co polypeptide or its fragment whose expression is inhibited by the

nucleic acid; (2) a host cell containing the vector; (3) an isolated

co polypeptide or its fragment whose expression is inhibited by the

co proliferation or the activity of a gene in an operon required for

proliferation; (7) identifying a compound that influences the activity of

required for proliferation, or that inhibits cellular proliferation; (8)

co proliferation; (7) identifying a compound that influences the activity of

required for proliferation, or that inhibits proliferation or the biological

corpused a gene required for cellular proliferation of an

corpused a gene required for cellular proliferation of an

corpused a gene required for cellular proliferation of an

corpused a gene required for cellular proliferation of an

corpused a gene on which the test compound that inhibits proliferation

compounds activity; (11) a culture comprising strains in which the gene

compounds activity; (11) a culture comprising strains in which the

compounds activity; (11) a culture compound that inhibits the

compounds activity; (11) a culture compound that inhibits the

crowning activity; (12) a compound that inhibits the

crowning activity; (13) dentifying the target of a compound that inhibits the

crowning proteins or screening for homologous nucleic acids are useful for

clear inflying proteins or screening for homologous nucleic acids required

contrains activity activity or activity and an interpression or and acids are useful for actional activity and activity and activity and activity and activity and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target profearyoric essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                            invention relates to an isolated nucleic acid comprising any
                              Claim 14; SEQ ID NO 7644; 1766pp; English.
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Sequence 984 BP; 399 A; 123 C; 181 G; 281 T; 0 U; 0 Other;

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                                                                            ValArgGlyLeuLysIleLeuSerValIleGlyLeuLeuPheValLeuIleAlaThrAla
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Conservative:
Mismatches:
Indels:
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861 ATCGCTGATAGCAGTAGACATAAAGGTATTAATAAGAATTAAACAAAATTGCACCAACA 420
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                                                                                                                                                                                                                                                                                      285 ProvalTrpLysLysLeuAsnAlaValLysAsnGlnArgValAspileLeuAspArgAsp
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                                                                   601 GTTGCTAAAGCTGGTTTATTAGCACATCCAAACTATTCATATGTTGGACAATTTTAAAC
                              205 AlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPheLeuSer
                                                                                                                                                                         GinLeuGlyPheLysGluAlaLeuSerAspAspValThrLysGlyLeuSerLysTyrLeu
                                                                                                                                                                                                           LysGlyProTyrLeuGlnMetAsnThrGluThrLeuSerGlnValAsnProGluArgMet
                   145 IleGluLeuLysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThrlle
                                                                                             185 ileGluGluTyrLysLysGluileThrMetAspLysAsnGlnLysValLeuProAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Staphylococcus aureus protein, useful as a vaccine for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis; enzymatic assay; antibiotic target; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                  LeuSerLysLysAspSerLys 331
                                                                                                                                                                                                                                                                                                                                                                             Scarselli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus aureus DNA #2666.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-MAR-2001; 2001GB-00007661
                                                                                                                                                                                                                                                                                                                                                                                                                           ACF74986 standard; DNA; 1044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; ABM73426
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English NO 5331; 49pp; 6; SEQ ID Claim

The invention relates to novel genes and encoded proteins from Staphylococcus aureus. A composition comprising the S. aureus protein, a nucleic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to Staphylococcus bacteria, specifically an infection caused by S. aureus. The composition is particularly useful for treating or preventing sepais in a patient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of novel S. aureus genes of the invention

Sequence 1044 BP; 425 A; 128 C; 191 G; 300 T; 0 U; 0 Other;

GlyValGluSerValArgGlyLeuLysIleLeuSerValIleGlyLeuLeuPheValLeu 1044 237 43 51 0 Length: Matches: Conservative: Mismatches: Indels: Gaps: US-10-724-972A-6352 (1-335) x ACF74986 (1-1044) 6.25e-108 1214.00 84.59\$ 71.60\$ Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores: н 41 No.: ò 셤 g õ ઠે g ઠે

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280 831 300 891 951 LeuAspArgAspLeuTrpAlaArgSerArgGlyLeulleSerSerGluGluMetAlaLys 320 SerLysTyrLeuLysGlyProTyrLeuGlnMetAsnThrGluThrLeuSerGlnValAsn ProgluArgMetPhelleMetThrAsnLysAlaSerSerAsnGluProSerLeuLysGlu jeuGluLysAspProValfrpLysLeuAsnAlaValLysAsnGlnArgValAspIle |||::::::||| TTACAAGAAGATGCAACATGGAAAAGTTGAATGCAGTTAAAAATAATGCGGGGGATATT Antisense; ds; prokaryotic cellular proliferation gene; antibiotic; antibacterial; drug design. Staphylococcus aureus DNA for cellular proliferation protein #239. 1012 GAACTIGTTGAATTATCAAAAAAGAACAAAAG 1044 331 GlubeuvalGlubeuSerbysbyspserbys ВР ; 2000US-0191078P. ; 2000US-020684BP. 2000US-020727P. ; 2000US-024257BP. ; 2000US-025362SP. ; 2000US-025731P. 21-MAR-2001; 2001WO-US009180 AAS51822 standard; DNA; 927 (first entry) (ELIT-) ELITRA PHARM INC. Staphylococcus aureus. de; WO200170955-A2 26-MAY-2000; 23-OCT-2000; 27-NOV-2000; 22-DEC-2000; 13-FEB-2002 21-MAR-2000; 23-MAY-2000; 16-FEB-2001; 27-SEP-2001 Antisense; 772 261 832 281 301 952 892 321 AAS51822 RESULT ò g ઠે a õ 요 ò 셤 δ g

The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia Coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify οŧ New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids. Claim 27; SEQ ID NO 4404; 511pp; English.

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Carr

Trawick JD,

Δ,

Wall

ď,

Zyskind

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Ohlsen Xu EE;

Haselbeck R, Yamamoto RT,

IleAlaProThrIleGluLeuLy8SerPheAspGlyAspTyrAsnGluAsnIleAspAla 160

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PhelysThrileSerbysAlaLeuGlyLysGluGluGluGluGlyLysLysArgLeuGluGlu 180

HisAspLysLysljeGluGluTyrLysLysGluIleThrMetAspLysAsnGlnLysVal 200

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LeuProAlaValAlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGly 220

GlnPheLeuSerGlnLeuGlyPheLysGluAlaLeuSerAspAspValThrLysGlyLeu 240

WPI; 2001-611495/70. P-PSDB; AAU33963

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antibodies capable of binding to the expresse these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LysaspieuAsniysilealaProThrIleGluLeuLysSerPheAspGlyAspTyrAsn 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      541 AGAAATCAAAAAGTGCTTCCAGCAGTTGTTGCTAAAGCTGGTTATTAGCACATCGAAAC
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                                                                                                                                    Sequence 927 BP; 370 A; 120 C; 169 G; 268 T; 0 U; 0 Other;
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Matches:
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Mismatches:
Indels:
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes con their use in the discovery of novel antibiotics, the essential genes at the protection of proteins. The prokaryotes used are Escherichia to the staphylococcus aureus, Salmonalla typhi, Klebbiela pneumoniae, con sedul for the identification of potential new targets for antibiotic cuseful for the identification of potential new targets for antibiotic con tribodies capable of binding to the expressed proteins, and to obtain contributes used in proliferation, to express these proteins and to obtain contibents used in proliferation, to express these proteins and to obtain contibents and to state of antibenes and sequence is also useful to screen for homologous contisense nucleic acid sequence encodes an essential prokaryotic of organisms. The present sequence encodes an essential prokaryotic of organisms. The present sequence encodes an essential prokaryotic collular proliferation protein. Note: The sequence date for this patent coll not form part of the printed specification, but was obtained in clear electronic format directly from WIPO at
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                                                                                        TTAGCTGACTTAAATCCTGAACGCATGATTATTATGACAGATAATGCTAAAAAAGATTCT
                                                ProSerLeuLysGluLeuGluLysAspProValTrpLysLysLeuAsnAlaValLysAsn
                                                                                                                                                                                                                                                                                                                                                        prokaryotic cellular proliferation gene; antibiotic; drug design.
                                                                                                                                                                                                                                                                                                                                 cellular proliferation protein #29.
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2000US-0206848P.
2000US-0207727P.
2000US-0242578P.
2000US-0253625P.
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2001US-0269308P.
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26-MAY-2000; 2
23-OCT-2000; 2
27-NOV-2000; 2
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16-FEB-2001; 2
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Alignment Scores 셤 8 용 114 174 105 GlyThrArgLysGlnProAsnLeuGluGluIleSerLysLeuLysProAspLeuIleIle 125 354 126 AlaAspAsnAsgHisLysGlyileTyrLysAspLeuAsnLysIleAlaProThrile 145 414 474 LysalaleuglyLysgluglugluglyLysLysargleuglugluHisaspLyslle 185 234 294 GluLeuLysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThrIleSer 165 69 45 65 85 226 LeuGlyPheLysGluAlaLeuSerAspAspValThrLysGlyLeuSerLysTyrLeuLys 245 654 GlyProTyrLeuGlnMetAsnThrGluThrLeuSerGlnValAsnProGluArgMetPhe 265 266 IleMetThrAsn---LysAlaSerSerAsnGluProSerLeuLysGluLeuGluLysAsp 284 ArgGlyLeuLys1leLeuServal1leGlyLeuLeuPheValLeu1leAlaThrAlaAla СүвGlүАвпАвпSerSerAвпSerSerLyвGluSerSerLyвAвpGlyValGluIle ||||||| 70 TGTGGTCAAAAGATACT------GAAGAGAAAACTGAAATGACGACAATA LysHisGluGluGlyThrThrLysValProLysHisProLysArgValValLeuGlu 295 GGATCTAGACCGCACCGAATATGGAAGTGATAAAGTAAAATTAAAACCGGATTTGATCATA GluGluTyrLysLysGluIleThrMetAspLysAsnGlnLysValLeuProAlaValAla 535 GCGGAGATTAGAAAGAAAATTGAACAGAGTACGTTAAAAAACTGCATTTGCATTCGGTATC AlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPheLeuSerGln U; 0 Other; **:: ||||::: |||| TTAGCCACTGACGGAAAACGACAAAATAGAACGAAATTC------957 153 61 99 12 Length:
Matches:
Conservative:
Mismatches:
Indels: 0 :-Sequence 957 BP; 382 A; 114 C; 209 G; 252 US-10-724-972A-6352 (1-335) x AAS51612 (1-957) ftp.wipo.int/pub/published_pct_sequences 726.00 65.85% 47.08% 42.96% Percent Similarity: Best Local Similarity: Scores: 106 26 46 115 146 655 355 415 166 475 186 506 246 715 Query Match: DB: 823 Alignment g Pred. No.: Score: SXS ઠે 셤 요 ઠ ઠે 셤 ે 8 S පු ઠે ద ઠે 엄 ઠે g g ઠે 8 8 6 8 6 8 6 g ઠે 셤 ò

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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of movel antibiotics, the essential genes their use in the discovery of movel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonalla typhi, Klebbiella pneumoniae, CC seeddomonas aeruginosa and Enterococcus faccalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain compounds in rational drug discovery programmes. The autisense nucleic acids sequence is also useful to screen for homologous contisens acid sequence is also useful to screen for homologous contisens acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent contine format directly from WIPO at the contine format directly from WIPO at the contine format directly from WIPO at the contine format directly from WIPO at
                                   AspLeuTrpAlaArgSerArgGlyLeuIleSerSerGluGluMetAlaLysGluLeuVal 323
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antibacterial; drug design.
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Xu HH;
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23-MAY-2000; 2000US-0206848P.
25-MAY-2000; 2000US-020727P.
23-OCT-2000; 2000US-0242578P.
27-NOV-2000; 2000US-0253625P.
22-DEC-2000; 2000US-0257931P.
16-FEB-2001; 2001US-0269308P.
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                                                                                                                                                            943 AAAATTGCAGAAAAA
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                                                                                 ArgGlyLeuLysIleLeuSerValIleGlyLeuLeuPheValLeuIleAlaThrAlaAla
                                                                                                                        CysGlyAsnAsnSerSerAsnSerSerLysGluSerSerLysAspGlyValGluile
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          Matches:
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Mismatches:
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Gaps:
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The invention relates to a novel method for identifying, isolating and producing hyperimmune serum-reactive antigens from a pathogen, tumour, producing hyperimmune serum-reactive antigens from a pathogen, a tissue or host prone to auto-immunity, where the antigens are pool of a type of animal, or individual sera with antibodies against the pool of a type of animal, or individual sera with antibodies against the pool of a type of animal, or individual sera with antibodies against the pool of a type of animal, or individual sera with antibodies against the configuration and the serum-reactive antigens comprising any of the immunity. The hyperimmune serum-reactive antigens comprising any of the immunity. The hyperimmune fragments are useful for the manufacture of a pharmaceutical preparation, against S. aureus or S. epidermidis. The infections or colonisation against S. aureus or S. epidermidis. The corporation of antibodies is useful for the manufacture of a medicament of preparation of antibodies is useful for the manufacture of a medicament or search or preventing staphylococcal infections or colonisation caused for diagnostic and imaging purposes. Other conditions may also be used for diagnostic and imaging purposes. Other conditions that can be treated include cancer, autoimmune diseases or infections caused by viral (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This method for identifying and producing pathogen specific antigens of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying, isolating and producing hyperimmune serum-reactive antigen
from a pathogen, for preparing vaccine or medicament for treating or
preventing e.g. staphylococcal infections, comprises providing antibody
                                                                                                                                                                                                                                                                                Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV; hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen; auto-immunity; vaccine; staphylococcal infection; antibody; cancer; autoimmune disease; HIV; hepatitis; gene; ds.
                                                                                                                                                                                                                                         Pathogen specific antigen related staphylococcal DNA SEQ ID No 301.
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Hafner
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Etz H, Dryla A, Weichhart T,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
                                                                                                                       BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-JAN-2001; 2001AT-00000130.
324 GluLeuSerLysLys 328
                                         951
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                         937 AAAATTGCAGAAAAA
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Minh DB, Vytvytska O,
Tempelmaier B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-075410/07.
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U; 0 Other;

BP; 383 A; 116 C; 210 G; 248 T; 0

Sequence 957 Alignment Scores:

invention

957 149 63 95 11

Matches: Conservative: Mismatches: Indels:

1.34e-60 724.50 66.67% 46.86% 42.87%

Best Local Similarity:

Query Match:

Percent Similarity

prokaryotic essential gene; cell proliferation;

gene #1736.

(first entry)

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21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00572851.
06-MAR-2002; 2002US-0362699P.
                                                                                                21-MAR-2002; 2002WO-US009107
                                                                                                                                                        (ELIT-) ELITRA PHARM INC.
                     Prokaryotic essential
                                                       Staphylococcus aureus.
                                                                                                                                                                                          WPI; 2003-029926/02.
P-PSDB; ABU16209.
                                  Antisense; ds; prok
drug design; gene.
                                                                     WO200277183-A2.
       19-JUN-2003
                                                                                   03-OCT-2002.
                                                                                                                                                                      Wang L,
Wall D,
152
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Zyskind X

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Ohlsen | Forsyth |

Haselbeck R, Yamamoto R,

Malone C, Carr GJ,

Zamudio C, Trawick JD,

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibites proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid

(1) a vector comprising a promoter operably linked to the antisense

(2) a host cell containing the but the antisense

(3) an isolated

(4) a nest call containing the but the antisense

(5) polypeptide (5) production the polypeptide by the antisense

(6) polypeptide (5) producting the polypeptide; (6) inhibiting cellular

(7) contiferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation, or that inhibits cellular proliferation; (8)

(8) the gene product or that has an activity against a balological pathway in which a proliferation-required gene or its gene product is the area of a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound; a activity; (11) a culture comprising strains in which the gene or grading acts; (9) manufacturing an antibiotic; (10) profiling a compound; a activity; (11) a culture comparising strains in which the strains; or (13) identifying the excenting for monitoric acids required for orbiliferation of an organism. The antisense nucleic acids required for callular proliferation in cells other than S. auteus, S. typhimumian, C. for callular proliferation in cells other than S. areas, S. typhimumian, C. for callular proliferation in cells other than S. areas, S. typhimumian, C. functional agencies not be proliferation in cells other than S. areas, S. typhimumian, C. functional agencies Note: The sequence is one of the target prokaryotic essential gene necessary programs, or for screening for measures, S. typhimumian, C. functional directly from WIPO at the requence of the printed specification, but was obtained in the form part of the pri New antisense nucleic acids, useful for identifying proteins or s for homologous nucleic acids required for cellular proliferation isolate candidate molecules for rational drug discovery programs. Claim 14; SEQ ID NO 7949; 1766pp; English. BP; 385 A; 115 C; 210 G; 250

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standard; DNA; 960

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ACF74415 standard; DNA; 975

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                                                                                                                                                                                                                                             LeuGluGluIleSerLysLeuLysProAspLeuIleIleAlaAspAsnAsnArgHisLys 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                       <u> aaaatcaaattgagcaaattgctccgacaatcatcatatagtagcaaggaa</u>
                                                               ValileGlyLeuLeuPheValLeuIleAlaThrAlaAlaCysGlyAsnAsnSerSer
                                                                                                 AsnSerSerLysGluSerSerLysAspGlyValGluIleLysHisGluGluGlyThrThr
                                                                                                                                    LysvalProLysHisProLysArgvalvalvalLeuGluTyrSerPheValAspAlaLeu
                                                                                                                                                                       ValAlaLeuAspValLysProvalGlyIleAlaAspAspAsnLysLysAsnArglleIle
                                                                          GlyLeuileSerSerGluGluMetAlaLysGluLeuValGluLeuSerLysLys 328
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   Conservative:
           Mismatches:
Indels:
Gaps:
                                                (1-335) x ACA20079 (1-960)
    66.67%
46.86%
42.87%
     Similarity:
                                                  US-10-724-972A-6352
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The invention relates to movel genes and encoded proteins from Staphylococcus aureus. A composition comprising the S. aureus protein, a nucleic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to Staphylococcus bacteria, specifically an infection caused by S. aureus. The composition is particularly useful for treating or preventing sepsis in a patient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic atudies and as a target for antibiotics. This sequence represents one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ģ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33 AsnSerSerLyaGluSerSerLyaAspGlyValGluileLysHisGluGluGluGlyThrThr
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enzymatic assay; antibiotic target; gene; ds.
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Mismatches:
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aureus DNA #2095
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66.67%
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                                                                                                      Staphylococcus aureus
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Best Local Similarity:
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D-SQUARED BIOTECHNOLOGIES INC

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Novel surface-exposed immunogenic polypeptide of Staphylococcus aureus containing receptors for siderophores or iron-binding ligands, useful producing antibodies effective against Staphylococci infection.
              17-JUN-2002; 2002WO-US019224
                            17-JUN-2001; 2001US-0298975P
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LysProLeuArgAspLysIleGlyLysTyrThrSerValGlyThrArgLysGlnProAsn
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                                                            Gly11eTyrLysAspleuAsnLys1leAlaProThr11eGluLeuLysSerPheAspGly
                                                                     HisProSerAsnSerTyrValGlyGlnPheLeuSerGlnLeuGlyPheLysGluAlaLeu
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                                                                                                                                                                                                                                                     ThrGluThrLeuSerGlnValAgnProGluArgMetPheIleMetThrAsn---LygAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Surface-exposed immunogenic polypeptide; SEIP; siderophore; receptor;
                                                                                                                                                                                                                                                                                                                                                  Staphylococcal surface-exposed immunogenic polypeptide DNA
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/product= "SEIP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus.
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                                  The present sequence is that of DNA encoding novel Staphylococcus aureus surface-exposed immunogenic polypeptide (SEIP) D2 SA05. To isolate SEIP genes, an expression library of S. aureus genomic DNA was screened with anti-SEIP antisera. DNA was isolated from clones expressing SEIPs, and amino acid sequences were deduced and analysed for conserved and/or sequence homology with the SEIP encoded by the present DNA sequence has sequence homology with the siderophora family of periplasmic binding proteins. The invention provides methods for the identification, in combination, to produce anti-staphylococcal antibodies used individually, or passive or active immunisation strategies to prevent or contain standylococcal infection. They can also be used to develop diagnostic
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                                                                                                                                                                                                                                                                                                                             Sequence 2957 BP; 1160 A; 381 C; 512 G; 904 T; 0 U; 0 Other;
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Matches:
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Claim 4; Page 55-56; 62pp; English.
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Best Local Similarity:
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                                                         Alignment Scores:
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                                   AsnalavallysAsnGlnArgvalAspileLeuAspArgAspLeuTrpAlaArgSerArg 310
                                                          212
                                                                                                                                                             ThrGluThrLeuSerGlnValAsnProGluArgMetPheIleMetThrAsn---LysAla 271
                                                                                                                                                                                              SerSerAsnGluProSerLeuLysGluLeuGluLysAspPro---ValTrpLysLysLeu 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence encodes a novel polypeptide, which is optionally expressed in NCIMB 40771. The polypeptide, and polynucleotide encoding it, are derived from Staphylococcus aureus. Calls expressing ligands binding the polypeptide can be used to isolated candidate compounds that
                                                                                                                                                                                                                                          1838 AAAGCIGIGAAAGAIAACAAAGIITAIGACGIIGAACGAAAIAAGIGGIIGAAAICAAGG
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1550 GAACAGAGTACGTTAAAATCTGCATTTGCATTCGGTATCTCAAGAGCAGGTATGTTTATT
                                                                                                                            SerAspAspValThrLysGlyLeuSerLysTyrLeuLysGlyProTyrLeuGlnMetAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New Staphylococcus aureus polynucleotide and polypeptide(s) - for isolating antagonist of the polypeptide(s) useful as anti-bacterials
                                                          193 ThrMetAspLysAsnGlnLysValLeuProAlaValAlaAlaLysSerGlyLeuLeuAla
                          GluGlyLysLysLysLysLeuGluGluHisAspLysLysIleGluGluTyrLysLysGluIle
                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus aureus WCUH 29; antagonist; antibacterial; immunogen; vaccine; disease; protection; isolation; 8s.
                                                                                                                                                                                                                                                                          GlyLeuIleSerSerGluGluMetAlaLysGluLeuValGluLeuSerLysLys 328
                                                                                                                                                                                                                                                                                                                                                                     encoding cDNA sequence
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                                                                                                                                                                                                                                                                                                                     AAT80398 standard; cDNA; 2247
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  bind and inhibit the activity of the polypeptide. Such compounds can be
used as anti-bacterial compounds. The polypeptide may also be used as
immunogen to vaccinate an animal for protection against Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeulysProAspleuileileAlaAspAsnAsnArgHisLysGlyileTyrLysAspleu
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ttgggggt-aatacttctgtaggtacacgtaa-caagcnaacttaagaganattagtaaa
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| AGATACTAITTCGGGTAAAGATGAAAAGGTACAGTAAAAGTACCTAAAGATGCACAAC
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Matches:
Conservative:
Mismatches:
                                                                      Sequence 2247 BP; 704 A; 397 C; 307 G; 802
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PHI:7000-87/6-17/ OT 0
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The present sequence encodes 3 Staphylococcus aureus proteins of unknown function. The present sequence was isolated from a library of clones of S. aureus WCUH 29 in Escherichia coli. The DNA sequence can be used in the construction of ribozymes and antisense sequences to control the expression of Staphylococcal genes. The DNA sequence is also useful as a source of regulatory elements for the control of bacterial gene expression. The encoded protein may be used to produce vaccines to enable a host to produce specific antibodies with antibacterial action. These vaccines and antibodies would protect a host against invasion by S. sureus, and conditions relating to Staphylococcal infection, e.g. Staphylococcal food poisoning, scaled skin syndrome, and toxic shock
                                                                                                                                              Staphylococcus aureus protein; ribozyme; antisense sequence; control; Staphylococcal gene; regulatory element; baccerial gene expression; vaccine; Staphylococcal infection; food poisoning; scaled skin syndrome; toxic shock syndrome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel polypeptide(s) from Staphylococcus aureus strain WCUH29 - used to isolate antimicrobial compounds, and in vaccines against S. aureus
                                                                                                              DNA encoding 3 Staphylococcus aureus proteins of unknown function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Black MT, Burnham MK, Hodgson JE, Knowles DJC, Nicholas RO;
Pratt JM, Reichard RW, Rosenberg M, Ward JM;
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complement(1705. .2016)
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complement(1456. .1587)
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AAT83786/c
ID AAT83786 standard; DNA; 2247 BP.
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                                                                              16-JUL-1998 (first entry)
                                                                                                                                                                                                                             Staphylococcus aureus.
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Sequence 2247 BP; 704 A; 397 C; 307 G; 802 T; 0 U; 37 Other;

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         Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
       8.49e-60
721.00
73.48%
60.57%
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                    Percent Similarity:
Best Local Similarity:
Query Match:
Alignment Scores:
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1 GlyValGluSerValArgGlyLeuLysIleLeuSerValIleGlyLeuLeuPheValLeu 20

US-10-724-972A-6352 (1-335) x AAT83786 (1-2247)

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g	771	CTTTAGTTGCAGCTTGTGGTAATACGGATAATTCAAGTAAAAGAAGAATCATCAACTAA 712
g 4	711	ProLysHisProLysA 6
o S	651	AlaLeuAspValLysp 79 ::: CATATAGCCGTTANAC 59:
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RESU ADF3 ID XX	3ULT 16 ?30765/c ADF30765	
XX	ADF3076	
E X	12-FEB-2004 (first entr)	
X	Bacillus subtilis strain MB1510 inte	egration region DNA SEQ ID NO:20.
X X X	W expression library, Gram-positive ba W non-replicating linear integration c	ıcterium host cell; assette; gene; Bacillus; ds.
s x	S Bacillus subtilis. X	
N X	N WO2003095658-A1.	
<u>B</u>	D 20-NOV-2003.	

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07-MAY-2003; 2003WO-DK000301.

07-MAY-2002; 2002DK-0000682.

(NOVO ) NOVOZYMES AS.

Bjornvad ME, Jorgensen PL, Hansen PK;

WPI; 2004-012127/01.
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Generating an expression library of polynuclectides by introducing the linear integration cassette into the host cell and selecting or screening for host cells that produce the polypeptides of interest.

gxample 5; SEQ ID NO 20; 55pp; English.

The present invention describes a method for generating an expression CC library of polymuclectides integrated by homologous recombination into the genome of a competent Gram-positive bacterium host cell. The method cc comprises: (a) providing a non-replicating linear integration cassette: The method cc comprises: (a) a polymucleotide the polymetides cc and selecting or screening for host cells that produce the polymetides cc interest. The cassette comprises: (a) a polymucleotide encoding one or of interest. The cassette comprises: (a) a polymucleotide segment copprise of the polymucleotide of (l) and comprising a first homologous copprising a first homologous region located in the 3' end of the polymucleotide of (l) and comprising a second homologous region located in the 5' end of the polymucleotide of (l) and comprising a second homologous region located in the 5' end of the segment. The first and second homologous regions are at least 80, 1000 cr 1500 bp, each of which has a sequence identity of at least 80, 85, 90 cr 1500 bp, each of which has a sequence identity of at least 80, 85, 90 cr 1500 bp, each of which has used cell genome. Also described: (l) a cor 1500 bp, with a region of the host cell genome. Also described: (l) a cor 25-100 with a region of the posticity of polymucleotides integrated by in generating an expression library of polymucleotides integrated by homologous recombination into the genome of a competent Gram-postivive cor present invention.

C strain MB1510 integration region, which is used in an example from the present invention.

Sequence 5718 BP; 1693 A; 1089 C; 1259 G; 1677 T; 0 U; 0 Other;

Alignment Scores: 2.84e-55 Length: 5718
Pred. No.: 679.50 Matches: 149
Score: 62.78* Conservative: 50
Best Local Similarity: 47.00* Mismatches: 103
Query Match: 12 Gaps: 4
DB:

US-10-724-972A-6352 (1-335) x ADF30765 (1-5718)

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                                                                                                                                                                                                                                                                                 268 ThrasnLysalaSerSerAsnGluProSerLeuLysGluLeuGluLysaasproValTrp 287
                                                                                                                                                              PhelysGluhlaLeuSerAspAspValThrLysGlyLeuSerLysTyrLeuLysGlyPro 247
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                                                                                                                                                188 TyriysiysGjuileThrMetAspLysAsnGlnLysValLeuProAlaValAlaAlaLys
                                                                                                                                                                                                                                                                     TyrLeuGlnMetAsnThrGluThrLeuSerGlnValAsnProGluArgMetPheIleMet
                                                                                                                        SerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPheLeuSerGlnLeuGly
                              128 AsnAsnArgHisLysGlyIleTyrLysAspLeuAsnLysIleAlaProThrIleGluLeu
                                                                     LysserPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThrIleSerLysAla
                                                                                gcrgagcigccaraaaaacarrraraaacagcrgaaaaaaaarcgccccgacgarrgaarra
                                                                                                                                                                                                                                                                                                                                                                                         ArgserArgGlyLeulleSerSerGluGluMetAlaLysGluLeuValGlu 324
                                                                                                                                                                                                                                                                                                                                                                                                      Antisense; ds; prokaryotic essential gene; cell proliferation;
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TTTACACACGCTGTGAAGTCAGAT------
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06-SEP-2001, 2001US-00948993.
25-CCT-2001, 2001US-0342953.
08-FEB-2002; 2002US-0362699P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus haemolyticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACA47237 standard; DNA; 525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    drug design; gene.
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241 GGGGTTGCTGATGACAACAAACCAAATCGTATTATTAAACCATTAAAAGAAAAATTGGA 300

Trawick JD, WPI; 2003-029926/02. P-PSDB; ABU43367. ۵ Wall

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Forsyth RA,

Yamamoto R,

Carr GJ,

New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

Claim 14; SEQ ID NO 35107; 1766pp; English.

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression to the 6213 antisense sequences given in the specification where expression (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) an best cell containing the vector; (3) an isolated of antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for the pense product or that has an activity against a biological pathway in which a proliferation-required gene product lise crequired for proliferation, or that inhibits cellular proliferation of an identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or the biological pathway in which a proliferation-required gene or tis gene product lise or a gene on which the test compound that inhibits proliferation of an compound sactivity; (11) a culture comprising strains in which the extent or operation of an organism activity; (12) a culture comprising strains in which the extent or which each of the strains is present in a culture or collection of proliferation of an organism. The antisense nucleic acids required for proliferation to isolate candidate molecules for rational required for proliferation in cells of a compound that inhibits the contiferation of an organism. The present sequence data for this patent did required for proliferation to isolate candidate. Sequence is one of the target of proveryprograms, or for screening homologous nucleic acids required for proliferation in cells order than S. auteurs, s. typhimmrium, or the printed for proliferation to isolate candidate. Sequence data for this patent did celectronic format directly from Windows.

Sequence 525 BP; 200 A; 66 C; 96 G; 163 T; 0 U; 0 Other;

Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 3.91e-53 644.00 84.00% 70.86% 38.11% Percent Similarity: Best Local Similarity: Query Match: DB:

521 234 44 14 14 14

US-10-724-972A-6352 (1-335) x ACA47237 (1-525)

5 ValArgGlyLewLysIleLeuSerValIleGlyLeuLeuPheValLeuIleAlaThrAla 24 AlaCysGlyAsnAsnSerSerSerAsnSer------SerLysGluSerSerLys 40 25 g ઠે ઠે g ઠે

AspGlyValGluIleLysHisGluGluGlyThrThrLysValProLysHisProLysArg 60

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301 GATTATAAATCTGTTGGTGCTCGTAAACAACCCAACTTAGAAGAAATCAGTAAATTAAAA 360 ileAlaProThrileGluLeuLysSerPheAspGlyAspTyrAsnGluAsnIleAspAla 160 ProAspLeullelleAlaAspAsnAsnArgHisLysGly1leTyrLysAspLeuAsnLys 101 LysTyrThrSerValGlyThrArgLysGlnProAsnLeuGluGluIleSerLysLeuLys ds; prokaryotic essential gene; cell proliferation; Prokaryotic essential gene #24493. ACA42836 standard; DNA; 897 BP. ; 2001US-00815242. ; 2001US-00948993. ; 2001US-0342923P. ; 2002US-00072851. ; 2002US-0362699P. 21-MAR-2002; 2002WO-US009107 (first entry) (ELIT-) ELITRA PHARM INC. Pasteurella multocida. drug design; gene WO200277183-A2 06-SEP-2001; 25-OCT-2001; 08-FEB-2002; 19-JUN-2003 06-MAR-2002; 21-MAR-2001; 03-OCT-2002 121 141 ACA42836; RESULT 18 ACA4283 В δ g 셤 ઠે à ઠ

New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs. Zyskind JW; Xu HH; Haselbeck R, Ohlsen KL, Yamamoto R, Forsyth RA, Malone C, Carr GJ, Zamudio C, Trawick JD, WPI; 2003-029926/02. P-PSDB; ABU38966. ijĠ Wang Wall

Claim 14; SEQ ID NO 30706; 1766pp; English.

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense concleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular concerns the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological

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pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antiblocic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene or compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent or collection of conversed the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for proliferation of an organism. The candidate molecules for rational correquired for proliferation in calls other than S. aureus, S. typhimurium, crequired for proliferation in cells other than S. aureus, S. typhimurium, crequired for proliferation in cells other than S. aureus, S. typhimurium, broken proxem part of the printed specification, but was obtained in celectronic format directly from WIPO at clear for this patent did electronic format directly from WIPO at clear for this patent did for wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 897 BP; 293 A; 176 C; 195 G; 233 T; 0 U; 0 Other;
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897 111 65 98 17
Length: Matches: Conservative: Mismatches: Indels: Gaps:
1.67e-40 516.50 60.48% 38.14% 30.56%
Alignment Scores: Pred. No.: Score: Percent Similarity: Percent Similarity: Query Match:

US-10-724-972A-6352 (1-335) x ACA42836 (1-897)

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SerLysTyrLeuLysGlyProTyrLeuGlnMetAsnThrGluThrLeuSerGlnValAsn 260
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                                                                                               AlaAspAspAspLysLysAsnArgllelleLysProLeuArgAspLyslleGlyLysTyr 102
                      67 GTTACCGICAAAGATCAAAAAGGGGAATTTACCTTAGATAGCGTACCTAAACGTGTTGTT 126
                                                               127 GCCTIAGAAIATICTIAIGIGAIGCACIAGCACAAATIGGIGIGIGCCCGTIGGIGIG 186
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                                                63 ValLeuGluTyrSerPheValAspAlaLeuValAlaLeuAspValLysProValGlylle
                                                                                                             LeullelleAlaAspAsnAsnAsnArdHisLysGlylleTyrLysAspLeuAsnLysIleAla
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Monitoring differential expression of several genes in first Bacillus cell relative to expression of same genes in one or more second Bacillus cells, by using substrate containing Bacillus genomic sequenced tag
                                                                                         301 LeudapargdapLeuTrpalaArgSerArgGlyLeulleSerSerGluGluMetalaLys 320
ProGluArgMetPheIleMetThrAsnLysAlaSerSerAsnGluProSerLeuLysGlu 280
                                                                                                      802 GCTAATGATAATTTATGGGGAAGAGCACGTGGTATTGATGCCGGTGAAGTAATGGCTAAA 861
                 ||||:::|||| :::::::
|CCTGATCTGATGATCTTAATCCATTATCGT------GATGAGAGTATTGCAAGAAAA
                                             281 LeuGluLysaspProValTrpLysLysLeuAsnAlaValLysAsnGlnArgValAspIle
                                                                   742 TGGGAAAATGAAGCCTTATGGAAAATTATCCCTGCGGTAAAAAATGGTCAAGTCATCTTA
                                                                                                                                                                                                                                                                                                 tag; GST;
                                                                                                                                                                                                                                                                            Bacillus licheniformis genomic sequence tag (GST) #2066.
                                                                                                                                                                                                                                                                                                 Differential gene expression, genomic sequenced altered culture condition, environmental stress, physiological provocation; ds.
                                                                                                                                         321 GluLeuValGluLeuSerLysLysAspSerLys 331
                                                                                                                                                         Claim 4; SEQ ID NO 2066; 200pp; English.
                                                                                                                                                                                                              BP
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                                                                                                                                                                                                                                                                                                                                                                                                                    05-OCT-2001; 2001WO-US031437.
                                                                                                                                                                                                                                                                                                                                                                                                                                        06-OCT-2000; 2000US-00680598.
27-MAR-2001; 2001US-0279526P.
                                                                                                                                                                                                              ABK74775 standard; DNA; 801
                                                                                                                                                                                                                                                        13-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                Bacillus licheniformis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clausen IG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-416684/44.
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The invention describes a method of monitoring differential expression of genes in a first Bacillus cell relative to expression of the genes in cher Bacillus cells, comprising hybridising labelled nucleic acid probes cother Bacillus cells to a substrate containing array of Bacillus cells to a substrate containing array of Bacillus comported tags (GST) examining the array, and determining to relative gene expression by an observed hybridisation reporter signal of a spot in the array. The method is useful for measuring the expression of constraints in a first Bacillus cell relative to expression of the same genes con more second Bacillus cells. The method is useful for monitoring new companies in a first Bacillus cells. The method is useful for monitoring consistent acid for the condition of the same stability in dentitoring sene copy number variation and stability. Monitoring changes to in expression of genes may be used to provide a representation of the way companies may be used to provide a representation of the way companies are presentation of the particular cells adapt to changes in culture conditions.

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ACF70890 standard; DNA;

121-2/24-0332. End

(first entry)

20-NOV-2003

ACF70890;

100 GlyLygTyrThrSerValGlyThrArgLysGlnProAsnLeuGluGlulleSerLysLeu 119
123 AAAGGGTATACTTCAGTCGGTTCGCGCGCCCAGCCAAGCTTTGAAAAATTGCTTCTTA 182 This sequence represents a genomic sequence tag (GST) used in the method of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences 122 302 419 219 479 239 536 LysileAlaProThrileGluLeulysSerPheAspGlyAspTyrAsnGluAsnIleAsp 159 GluHisAspLysLysIleGluGluTyrLysLysGluIleThrMetAspLysAsnGlnLys 199 240 LeuSerLysTyrLeuLysGlyProTyrLeuGlnMetAsnThrGluThrLeuSerGlnVal 259 79 62 66 LysGluLeuGluLysAspProvalTrpLysLysLeuAsnAlavalLysAsnGlnArgval 298 agaccgatcgaaaagatcctctttggaaaagctcagcgcagtcaaaacgcaaggtt 716 80 ValGlylleAlaAspAspAspAsnLysLysAsnArglleIleLysProLeuArgAspLysIle GTCGGAATTGCGGACGAAACCTAAGTTTATTAACGAGAAAGGTCAGGGGAAAAATC ArgValValValLeuG]uTyrSerPheValAspAlaLeuValAlaLeuAspValLysFro :::||| 420 ATTCTTCTGGGGAACACAAATGAAGAAATCACCGTGCGCGATGAAACTTTTTCACG 200 ValleuProAlaValAlaAlaLy8SerGlyLeuLeuAlaHi8ProSerAsnSerTyrVal 220 GlyglnPheLeuSerGlnLeuGlyPheLysGluAlaLeuSerAspAspValThrLysGly 480 TCTCAGCTTCTGACGAAAATCGGCTATACATACGGTGTCGGAGACAGC---GGCAAAGGC GATGCCGAAAACGGTGAATCCGTCAATATTAAAATGACGCTCGAACAGCTGCTTGAGAAA AsnProGluArgMetPhelleMetThr---AsnLysAlaSerSerAsnGluProSerLeu AspileLeuAspArgAspLeuTrpAlaArgSerArgGlyLeuIleSerSerGluGluMet T; 0 U; 0 Other; 801 108 58 95 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: Sequence 801 BP; 257 A; 166 C; 204 G; 174 (1-801)US-10-724-972A-6352 (1-335) x ABK74775 5.54e-40 510.50 62.88% 40.91% 30.21% AlaLysGluLeu 322 | | | | ::: ATGGATGAAATC 788 Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores: ٣ 63 243 140 160 303 180 363 537 260 597 279 657 299 ខ្លួនខ្លួន ò 셤 ò ద ઠે ద ઠે ద ઠે 셤 셤 ઠે ઠે 8 & B 8 6 8 6 8 6 6 6 કે 8 ઠે

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The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences are sources of probes and primers for detecting the genome of P. luminescens of cources of probes and primers for detections to set of the genes. Antibodies (Ab) raised against the and related species, to study polymorphisms, for gene analysis and for detection/damplification of the genes. Antibodies (Ab) raised against the polypeptides encoded by the genes are used for detection/dentification of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that carry a gene-containing vector are used to select compounds that carry a gene-containing vector are used to five genes in plants, animals or microorganisms other than P. luminescens and are able to alter response or sensitivity to toxins and antibiotics produced by P. croominant production of the proteins, particularly toxins and cantibacterials useful as insecticides, bactericides and fungithat cantibacterials useful as insecticides, bactericides and fungithat care sensitive to P. luminescens and ab are also useful therespeutically (to treat microbial infection by bacteria or fungi that care sensitive to P. luminescens and the proteins are as virulence consensitive to the proteins are as virulence consensitive to the sensitive to the sense of the genes and the proteins are as virulence consensitive to the sense of the genes and whooping cough). This sequence represents one of the isolated P. luminescens genes
                                                                                                                                                                                                                                                                                                                                           Antibacterial, fungicide; insecticide; polymorphism; genetic analysis; detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biopesticide; virulence factor; disease model; plague; whooping cough; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 c sequence of Photorhabdus luminescens and encoded polypeptides e.g. as therapeutic antimicrobials and agricultural pesticides
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Length: Matches: Conservative: Mismatches: Indels:

1.42e-36 476.00 57.24% 36.04%

Percent Similarity: Best Local Similarity:

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----CATGCGGCAATGGTTTCTCTCAACCTGGAACAGTTACTGGCACTCAATCCTGAC 696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention comprises the amino acid and coding sequences of proteins from Photorhabdus luminescens which are active against insects. The proteins of the invention are toxic to Lepidoptera, specifically the genera Plutella, Helichia, Helicoverpa, Spodoptera and ostrinia. The DNA and protein sequences of the invention are useful in the preparation of transgenic, insect-resistant plants, specifically wheat and maize. The present Photorhabdus luminescens genomic DNA contains the coding sequence for the two insecticide proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid from Photorhabdus luminescens, useful for producing insecticidal polypeptides active against Lepidoptera, and for producing insect resistant transgenic plants.
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//product= "Photorhabdus luminescens insecticide"
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AGRONOMIQUE
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location/Qualifiers
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P-PSDB; ADR20889, ADR20891.
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(CNRS ) CNRS CENT NAT
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Query Match:
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Qy 143 ProThrIleGluLeuLyBSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLy8 162 Db 8207 CCTGTCGTGCTGCTGAAATCCGGAACGAAACTACGAAGAACTGCAATCTGCCGCG 8148 Qy 163 ThrIleSerLyBAlaLeuGlyLyGluGluGluGlyLyBArgLeuGluGluHisAsp 182 Db 8147 ATCATCGGCAAAGTCATGGGGAAGAGAGTGAGATCCAGAAACGGTCGCAAGACCGT B) 183 LyBLySIleGluGluTyrLyBLySLyBAGATGATCAGAAACGCTCAGTGCAAGACCGT C) 183 LyBLySIleGluGluTyrLyBLySLyBLyBAGATGACACAGAAGGCTCAGTGTGATTTT B) 8087 GAACGCATGAAAGGCTATGCCAGCCAGTTGCCACACAGGCTCAGTGTGTTTT C) 203 AlaValAlaAlaLySSerGlyLeuLeuAlaHi8ProSerAsmSerTyrValGlyGlnPhe 222 C) 11	Qy 223 LeuSerGlnLeuGlyPheLygGlualaLeuSerAspasPvalThrLygGlyLeuSerLyg 242 Db 7973 TTAACAGCATTAGGGCTAAAAGTTCCCGCATCAGTTAAT	RESULT 22 ACTEGATS 39 (GTAAAATC 7701 RESULT 22 CONTINUATION (10 of 57) of ACTEGATS from base 3900001 (Photorhabdus luminescens nucleoting Pragments Name Begin End ACTEGATS ACCESSION ACTEGATS (7 of ACTEGATS OF ACCESSION ACTEGATS OF ACCESSION ACTEGATS OF ACTEGATS OF ACCESSION ACCESSION

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                                              ds; prokaryotic essential gene; cell proliferation;
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342921P-
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P-
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                                                                                243 TyrLeuLysGlyProTyrLeuGlnMetAsnThrGluThrLeuSerGlnValAsnProGlu 262
                                                                                                                           ArgMetPhelleMetThrAsnLysAlaSerSerAsnGluProSerLeuLysGluLeuGlu 282
                                                                                                                                                                     LysAspProValTrpLysLysLeuAsnAlaValLysAsnGlnArgValAspIleLeuAsp 302
                                                                                                                                                                                                             ArgAspLeuTrpAlaArgSerArgGlyLeulleSerSerGluGluMetAlaLysGluLeu 322
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                                       LeuSerGlnLeuGlyPheLysGluAlaLeuSerAspAspValThrLysGlyLeuSerLys
                                                             TTAACAGCATTAGGGCTAAAAGTTCCCGCATCAGTTAAT---------
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Matches:
Conservative:
Mismatches:
Indels:
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Continuation (9 of 13) of
WP Sequence split into 13
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Yamamoto R,
  Carr GJ,
 Trawick JD,
                       WPI; 2003-029926/02.
P-PSDB; ABU28130.
Wall D,
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New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

SEQ ID NO 19870; 1766pp; English. Claim 14;

205 AlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPheLeuSer 224

IleGluGluTyrLysLysGluIleThrMetAspLysAsnGlnLysValLeuProAlaVal

g ઠે

ò 유 264 MetPheIleMetThrAsnLysAlaSerSerAsnGluProSerLeuLysGluLeuGluLys 283

694 CTGCTGGTTGCCCACTATCGC-----GAAGAGAGCATTGTTAAACGCTGGCAACAA

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284 AspProValTrpLysLysLeuAsnAlaValLysAsnGlnArgValAspIleLeuAspArg 303

603

SerLyshlaLeuGlyLysGluGluGluGlyLysLysArgLeuGluGluHisAspLysLys 184

165 370

185

310 ATTGCCGACAGCAGTCGCCATGCGGGATTTACACTGCCTTGCAGCAAATCGCGCCCGCTA 369

145 IleGluLeuLysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThrile

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Forsyth RA,

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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

Continuous a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated on the polypeptide; (5) producing the polypeptide; (5) producing the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular continuous proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway to the proliferation, (7) identifying a compound that inhibits proliferation of an operon required for proliferation, or that thas an activity against a biological pathway in which a proliferation-required gene product the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the proliferation-required gene or its gene product lies or a gene on which the proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an conganism acts; (9) manufacturing an antibiotic; (10) profiling a compound sectivity; (11) a culture comprising strains in which the gene or which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the colliferation of an organism. The antisense nucleic acids are useful for for scilleration of an organism. The antisense nucleic acids are useful for colliferation of an organism. The succession of active active active active active for proliferation of an organism. The present sequence is one of the target of creduit discovery programs, or for screening honologous nucleic acide active continuous or P acroginous proliferation in cells other than S aureus, S typhimuring content of the printed specification, but was ftp.wipo.int/pub/published_pct_sequences

U; 0 Other; Sequence 900 BP; 198 A; 266 C; 256 G; 180 T; 0

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AspAsnLysLysAsnArgilelleLysProLeuArgAspLysIleGlyLysTyrThrSer 104
                                                                                                                                                                                                  105 ValGlyThrArgLysGlnProAsnLeuGluGluIleSerLysLeuLysProAspLeuIle 124
                                                                                                                                                                                                                                           125 IleAlaAspAsnAsnArgHisLysGlylleTyrLysAspLeuAsnLysIleAlaProThr 144
                                                                                                      45 IleLysHisGluGluGlyThrThrLysValProLysHisProLysArgValValLeu
                                                                                                                   GITCAGGACGACGACGCITTACACTCGATAAAACGCCACAAGGGAITGIGGIGCIG
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            Length:
Matches:
Conservative:
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Indels:
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                                                                Gaps:
         4.95e-35
460.00
57.09%
35.82%
27.22%
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Percent Similarity:
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2000US-0206848P. 2000US-0207727P. 2000US-0242578P. 2000US-0253625P. 2000US-0257931P.

23-MAY-2000; 26-MAY-2000; 23-OCT-2000;

27-NOV-2000; 22-DEC-2000; 16-FEB-2001;

(ELIT-) ELITRA PHARM INC

2000US-0191078P

21-MAR-2000;

21-MAR-2001; 2001WO-US009180

27-SEP-2001

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304 AspLeuTrpAlaArgSerArgGlyLeulleSerSerGluGluMetAlaLysGluLeuval 323
        Antisense; ds; prokaryotic cellular proliferation gene; antibiotic; antibacterial; drug design.

    E. coli DNA for cellular proliferation protein #457.

                                                                  뗦.
                                                                 AAS52735 standard; DNA; 909
                                                                                          13-FEB-2002 (first entry)
                           GluLeu 325
                                     AAAATC 870
                                                                                                                                         Escherichia coli
                                                                                                                                                     WO200170955-A2.
              805
                           324
                                       865
                                                                               AAS52735;
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes their use in the discovery of novel antibiotics, the essential genes coll, Staphylococcus aureus, Salmonala typhi, Klebbiela pneumoniae, coll, Staphylococcus aureus, Salmonala typhi, Klebbiela pneumoniae, coll, Staphylococcus aureus, Salmonala typhi, Klebbiela pneumoniae, conseful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain contracts antisense nucleic acids captured for the expressed proteins. The proteins can in rational drug discovery programmes. The breast sequence encodes an essential prokaryotic of organisms. The present sequence encodes an essential prokaryotic collular proliferation protein. Note: The sequence data for this patent collular proliferation protein. Note: The sequence data for this patent collular proliferation protein. Note: The sequence data for this patent collular proliferation protein. Note: The sequence data for this patent collular proliferation protein. Note: The sequence data for this patent collular proliferation protein. Note: The sequence data for this patent collular proliferation protein. Note: The sequence data for this patent collular proliferation protein. Note: The sequence data for this patent collular proliferation protein. Note: The sequence data for this patent collular proliferation protein.
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Carr
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Trawick JD,
                                                                                                       New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids.
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                                                                                                                                                               Claim 27; SEQ ID NO 6372; 511pp; English
 Zyskind JW,
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460.00
57.45%
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   Ohlsen 1
Xu HH;
                                                       WPI; 2001-611495/70.
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Best Local Similarity:
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   Haselbeck R,
Yamamoto RT,
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                       609
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                                                                                                                                                                                  AspProValTrpLysLysLeuAsnAlaValLysAsnGlnArgValAspIleLeuAspArg
AlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPheLeuSer
                                                                                                                                     MetPhelleMetThrAsnLysAlaSerSerAsnGluProSerLeuLysGluLeuGluLys
                                                                                                                                                          CTGCTGGTTGCCCACTATCGC-----GAAGAGCATTGTTAAACGCTGGCAACAA
                                                                                                                                                                                                 Zyskind JW;
Xu HH;
                                            225 GlnLeuGlyPheLysGluAlaLeuSerAspAspValThrLysGlyLeuSerLysTyrLeu
                                                                  610 TCTCTGGGGCTG-----AACGTTCCCGCTGCGATG
                                                                                        LysGlyProTyrLeu---GlnMetAsnThrGluThrLeuSerGlnValAsnProGluArg
                                                                                                         AspLeuTrpAlaArgSerArgGlyLeuIleSerSerGluGluMetAlaLysGluLeuVal
                     ::: ::: S50 TCACGCGAACAGCAATTCAACTCAGAAGAGAGCTGGACCGGCAGCGTGCTGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antisense nucleic acids, useful for identifying proteins or E
for homologous nucleic acids required for cellular proliferation
isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Antisense, ds; prokaryotic essential gene; cell proliferation;
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Forsyth RA,
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14; SEQ ID NO 20621; 1766pp; English.
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Carr GJ,
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0042923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
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Trawick JD,
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435 184 IleGluGluTyrLysLysGluIleThrMetAspLysAsnGlnLysValLeuProAlaVal

SerLysAlaLeuGlyLysGluGluGluGlyGlyLysArgLeuGluGluHisAspLysLys

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cc (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense cucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide acid; (2) a host cell containing the vector; (3) an isolated autisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, or that has an activity against a biological pathway or proliferation, or that inhibits cellular proliferation; (8) identifying a gene product or that has an activity against a biological pathway in which a proliferation-required gene or its gene product is capanism acts; (9) manufacturing an antibiotic; (10) profiling a corpanism acts; (9) manufacturing an antibiotic; (10) profiling a product is overexpressed or underexpressed; (12) determining the extent compound that inhibits the proliferation of the strains is present in a culture or collection of product is overexpressed or underexpressed; (12) determining the extent compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for proliferation of an organism. The antisense nucleic acids required cor proliferation in cells other than S. aureus, S. typhimurium, corporating discovery programs, or for screening homologous nucleic acids for regional drug discovery programs, or for screening for homologous nucleic acids for required for proliferation in cells other than S. aureus, S. typhimurium, content form part of the printed specification, but was obtained in celectronic format directly from WIPO at the sequence of the printed specification, but was obtained in
                88888888888888888888888888888888888
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BP; 200 A; 262 C; 261 G; 186 T; 0 U; 0 Other; 909 100 62 104 16 Length: Matches: Conservative: Mismatches: Indels: Gaps: 5.01e-35 460.00 57.45\$ 35.46\$ 27.22\$ Percent Similarity: Best Local Similarity: Query Match: Alignment Scores:

(1-335) x ACA32751 (1-909) US-10-724-972A-6352

76 GITCAGGACGACGTTTACACTCGAAAAAACGCCACAACGGATTGTGGTGCTG 135 195 ValGlyThrargLysGlnProAsnLeuGluGluIleSerLysLeuLysProAspLeuIle 124 AspAsnLysLysAsnArgIleIleLysProLeuArgAspLysIleGlyLysTyrThrSer 104 llealaaapasnasnargHisLysGlyIleTyrLysAspLeuAsnLysIleAlaProThr 144 11eGluleulysserPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThrile 164 CIGCTGCTTAAGTCCCGCAACGAACCTACGCTGAAAATTTGCAATCTGCGGCTATCATC 435 SerLysAlaLeuGlyLysGluGluGluGlyLysLysArgLeuGluGluHisAspLysLys 184 64 84 45 IleLувніsGluGluGlyThrThrLувValProLyвНіsProLyвArgValvalValLeu IleGluGluTyrLysLysGluIleThrMetAspLysAsnGlnLysValLeuProAlaVal 65 136 85 196 105 256 125 316 145 376 165 196 ઠે g ઠે g ò g ઠે 요 ઠે g 8 ò 셤 કે 8

The invention relates to a method of identifying compounds that modulate a newly identified mar regulated (NIMR) polypeptide activity. The method comprises contacting an NIMR polypeptide with a test compound under interaction conditions, determining the ability of the compound to modulate the activity or expression of the polypeptide, and selecting the modulators. NIMR nucleic acids and polypeptides are used in the treatment of microbial infections, and in screening for modulators of NIMR expression and activity. These modulators can be used to reduce the infectivity of a microbe on a surface, and the virulence of a microbe in a subject suffering from an infection. AAS46232-AAS46278 represent

Disclosure; Page 178-184; 526pp; English

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MetPhelleMetThrAsnLysAlaSerSerAsnGluProSerLeuLysGluLeuGluLys 283
                                                                                                                     ::: ::: crgctrgctcactatcgc-----gaagagattgttaaacgctggcaacaa 750
                                                                                                                                                                   810
                                                                                                                                                                               mar regulated polypeptide; NIMR; microbial infection; antibacterial; ds.
            TCACGCGAACAGCAATTCAACCTGCATACTCAGGAGACCTGGACCGGCAGCGTGCTGGCC
                                                  205 AlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPheLeuSer
                                  GlnLeuGlyPheLysGluAlaLeuSerAspAspValThrLysGlyLeuSerLysTyrLeu
                                                                                  245 LysglyProTyrLeu---GlnMetAsnThrGluThrLeuSerGlnValAsnProGluArg
                                                                                                                                             AspProValTrpLysLysLeuAsnAlaValLysAsnGlnArgValAspIleLeuAspArg
                                                                                                                                                       Identifying compounds that modulate a newly identified mar regulated polypeptide activity, useful as antimicrobial compounds, involves contacting the polypeptide with a test compound.
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AAS46238 standard; DNA; 10244 BP.
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P-PSDB; AAU29336.
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ACA45366 standard; DNA; 891

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                                                                                                                                                                         11eLysHisGluGlyThrThrLysValProLysHisProLysArgValValLeu
                                                                                                                                                                                                                           GluTyrSerPheValAspAlaLeuValAlaLeuAspValLysProValGly1leAlaAsp
                      Sequence 10244 BP; 2347 A; 2737 C; 2791 G; 2369 T; 0 U; 0 Other;
Bacherichia coli NIMR coding sequences of the invention
                                                            10244
100
62
104
16
                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
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57.45%
35.46%
27.22%
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                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                     Alignment Scores:
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The invention relates to an isolated nucleic acid compirising any one of the 6213 antileanse sequences given in the specification where expression of the 6213 antileanse sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

CC (1) a vector comprising a promoter operably linked to the nucleic acid of the observation of antileanse expression is inhibited by the antisense concleic acid; (2) a host cell containing the vector; (3) an isolated continued by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the antisense cc proliferation or the activity of a gene in an operon required for proliferation, or that has an activity against a biological pathway the sequired for proliferation, or that has an activity against a biological pathway contained for proliferation, or that inhibits cellular proliferation; (8) required for cellular proliferation or the biological dentifying a gene required for cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling of an organism acts; (10) manufacturing an antibiotic; (10) profiling the extent or obliferation of the strains is present in a culture or collection of compound, activity; (11) a culture comprising strains in which the gene or underexpressed or underexpressed; (12) determining the extent or obliferation of an organism. The antisense nucleic acids required contains and organism. The antisense nucleic acids required contains and organism. The antisense nucleic acids required contains and proliferation of an organism. The antisense nucleic acids required contains and prover and address modeled are useful for an all was proliferation or the strains of an organism or screening for homologous nucleic soles required to a conditional activity; (10) activity in the proliferation or the strains or acceening for homologous nucleic soles required to a conditional activity and an organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antisense nucleic acids, useful for identifying proteins or scre
for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention relates to an isolated nucleic acid comprising any
                                                                                                                                                                      proliferation;
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Forsyth RA,
                                                                                                                                                                        prokaryotic essential gene; cell
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 14; SEQ ID NO 33236; 1766pp; English.
                                                                                                                                Prokaryotic essential gene #27023
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-2002; 2002WO-US009107
                                                                                       (first entry)
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Trawick JD,
                                                                                                                                                                                                                                                  Pseudomonas syringae.
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                                                                                                                                                                                                          drug design; gene.
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ftp.wipo.int/pub/published_pct_sequences

TrpAlaArgSerArgGlyLeuIleSerSerGluGluMetAlaLysGluLeuValGluLeu 325 Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV; hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen; auto-immunity; vaccine; staphylococcal infection; antibody; cancer; autoimmune disease; HIV; hepatitis; gene; ds. Pathogen specific antigen related staphylococcal DNA SEQ ID No 318. BP. ABT15032 standard; DNA; 990 (first entry) 326 SerLys 327 867 CTCAAG 06-MAR-2003 306 802 ABT15032; 862

WO200259148-A2

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01-AUG-2002

21-JAN-2002; 2002WO-EP000546.

26-JAN-2001; 2001AT-00000130.

Zauner W; Hafner M; C, Henics T, Weichhart T, U, Klade C Dryla A, Ahsen U, Etz H, Meinke A, Nagy E, Von Minh DB, Vytvytska O, Tempelmaier B;

WPI; 2003-075410/07.

Identifying, isolating and producing hyperimmune serum-reactive antigens from a pathogen, for preparing vaccine or medicament for treating or preventing e.g. staphylococcal infections, comprises providing antibody

Example 7; Page 210; 252pp; English.

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The invention relates to a novel method for identifying, isolating and producing hyperimmune serum-reactive antigens from a pathogen, tumour, callergen, a tissue or host prone to auto-immunity, where the antigens are used in a vaccine, comprises providing antibody preparation from a plasma of a type of animal, or individual sera with antibodies against the pool of a type of animal, or individual sera with antibodies against the comprise of a type of animal, or individual sera with antibodies against the immunity. The hyperimmune serum-reactive antigens comprising any of the contingual the preparation particularly a vaccine against staphylococcal infections or colonisation against staphylococcal infections or colonisation against staphylococcal infections or colonisation against staphylococcal infections or colonisation against staphylococcal infections or colonisation against can be used for diagnostic and imaging purposes. Other conditions that can be treated include cancer, autoimmune diseases or infections caused by viral continued include cancer, autoimmune diseases or infections caused by viral continued for identifying and producing pathogen specific antigens of the invention.

Sequence 990 BP; 398 A; 141 C; 179 G; 272

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This sequence represents Staphylococcus aureus cbrA DNA. The cbrA protein is predicted to have a molecular weight of about 36.8 kD and, along with cbrB (AAY42332) and cbbc (AAY42333), is thought to be involved in iron regulation, based on amino acid sequence homology with known iron regulation, based on amino acid sequence homology with known iron regulator proteins. S. aureus is a ubquircus pathogen which causes infections in burns, cellulitis, eyelid infections, food poisoning, joint infections in conjunctivitis, exceptions, skin infections, surgical wound infection, scalded skin syndrome and toxic shock syndrome. S. aureus is increasingly becoming resistant to known antibiotics, with methicillin-resistant S. aureus (MRSA) poses serious infection control problems, with the exception of the vancomyclin-type glycopeptide antibiotics. The protein may be useful to screen potential antagonists antibiotics. The protein may be useful to screen potential antagonists which could be used as antibiotics and it may be used as a vaccine to prevent or attenuate an infection caused by a member of the
925 TATAAATCTTCATTAAAACTTATTGACGATTTATATGAA-----AAGTTAAATATTGAA 978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus genus. The protein, or antibodies against it can be used in immunoassays to detect Staphylococcus in a biological sample. Probes and primers derived from the nucleic acid sequences may also be used to detect Staphylococcus nucleic acids in a biological sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus aureus genes and polypeptides, vectors and methods of
                                                                                                                                                                                                                                                                               detection; diagnosis; screening; antibiotic; resistance;
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P-PSDB; AAY42331.
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373 AAAGTTAGAAATGAAAAAGTTTACGATCAATTATCTAAAATCGCACCAACAGTT----- 426
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| TTAGTTAAAAAGACTGAAAGCGAATGGACTTCAAGTAAAGAGTGGAAAAATTTAGACGCA 870
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253 CAAAAACCGAAATTCGAATACATAAAAATGATTTAAAAGATACTAAGATTGTAGGTCAA
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541 TTCCAAAAA-------GATGCAAAGCAAAGTATAAAGATGCCATTGAAA
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589 GCTTCAGTTGTTAACTTCCGTGCTGATCATACAAGAATTTATGCTGGTGGATATGCTGGT
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LeulleSerSerGluGluMetAlaLysGluLeuValGluLeuSerLysLysAspSerLys
         New isolated Staphylococcus nucleic acid molecules, used to develop products for the diagnosis, prevention and treatment of Staphylococcal infections.
                                                                                                                             infection; therapy; diagnosis; vaccine; antibiotic;
                                                                                                              Staphylococcus aureus iron regulation gene cbrA.
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                                                                                                                                                                                                                                                                                         Choi GH;
                                                                                                                                   iron regulation; ss.
                                                                                                                                                                                                                                                                                                      WPI; 1999-562101/47.
P-PSDB; AAY31824.
                                                                                                                                                                                                                                      20-MAR-1998;
01-APR-1998;
07-MAY-1998;
                                                                                                                                                                                                                                                                                         Simpson AJG,
                                                                                                 06-DEC-1999
                                                                                                                                                                                             WO9947639-A2
                                                                                                                                                                                                                         19-MAR-1999;
                                                                                                                                                                                                           23-SEP-1999.
                                                                                                                             CbrA gene;
312
                                                                                   AAZ19889;
                           332
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                                                             AAZ19889
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Claim 1; Page 24; 102pp; English.

This is the nucleotide sequence of Staphylococcus aureus strain ISP3

(ATCZ 202108) genomic DNA including the novel cbrA gene that codes for a 310-amino acid protein (see AAY1824) of predicted mol.wt. 36.8 kDa. The sequence was obtained from overlapping clones BTACA44 and BTAGU54, which AAD1889-91). CbrA shows sequence homology to known genes involved in iron regulation. The invention provides 11 novel genes (see AAX1889-92) of S. aureus and the polypeptides they encode (see AAX18181-27). Also provided are vectors, host cells, antibodies and hybridomas. The invention further relates to screening methods for identifying agonists and antagonists of S. aureus polypeptide activity, and to diagnostic methods for detecting Staphylococcus nucleic acids, polypeptides and antibodies in a biological sample. Antagonists of cbrA may be useful as antibodies in a biological sample. Antagonists of cbrA may be useful as antibotics to treat infections of S. aureus and other Staphylococcus spp. Infection by Staphylococcus. The isolated nucleic acid molecule is also broduction of cbrA protein

Sequence 999 BP; 402 A; 142 C; 180 G; 275 T; 0 U; 0 Other;

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                                                                                                                                                                                               193 GCCACTGACGTCGCTGTATCTTTAGGTGTTAAACCTGTAGGTGCTGTAGAATCATGGACA 252
                                                                                                                                                                                                                 LysAsnArgIleIleLysProLeuArgAspLysIleGlyLysTyrThrSerValGlyThr 107
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                                                                                                                                                                                                                                                  108 ArgLysGlnProAsnLeuGluGluIleSerLysLeuLysProAspLeuIleIleAlaAsp 127
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|GGGAATTCAAATAACAATCATCTCGATAACAAAGATAAGGAAACAACTTCAATTAAACAT 132
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                                                                                                                                               GluGluGlyThrThrLysValProLysHisProLysArgValValValLeuGluTyrSer 67
                                                                                                                                                                               PheValaspAlaLeuValAlaLeuAspValLysProValGlyIleAlaAspAspLys 87
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                                                                                       GlnValAgnProGluArgMetPhelleMetThrAsnLysAlaSerSerAsnGluProSer
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34
    Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                             US-10-724-972A-6352 (1-335) x AAZ19889 (1-999)
                                               Gaps:
   1.19e-29
405.00
51.74%
32.85%
23.96%
                    Percent Similarity:
Best Local Similarity:
Query Match:
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Alignment Scores
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The invention describes a new isolated nucleic acid molecule comprising: a sequence that is 95% identical to a fully defined sequence having 586-226 bp, or its complement; or a sequence encoding a polypeptide having a fully defined sequence comprising 136-691 amino acids, or its complement. The gene is Staphylococcus aureus gene. The nucleic acid is useful for preventing or attenuating an infection caused by a Staphylococcus, detecting Staphylococcus nucleic acids in a biological sample obtained from an animal, and detecting Staphylococcus antibodies in a biological sample obtained from an animal. This sequence
                       331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Staphylococcus aureus gene, useful for preparing a vaccine against infection caused by Staphylococcus aureus.
LeulleSerSerGluGluMetAlaLysGluLeuValGluLeuSerLysLysAspSerLys
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                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus aureus infection, infection prevention; infection attenuation; gene; ds; cbrA.
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
7. .999
/*tag= a
/product= "cbrA"
                                                                                                                                                                                                                                                                                                                                   Staphylococcus aureus cbtrA DNA
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98US-0080296P.
98US-0084674P.
99WO-US006199.
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                                                                                                                                                                                                             standard; DNA; 999
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                                                                                        LysAspAsnLys 335
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                                                                                                                        985 AAACAATCAAAA
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P-PSDB; ADF43556.
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Best Local Similarity:
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01-APR-1998;
07-MAY-1998;
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atch: 23.96% Indels: 34 10 Gaps: 12	24-972A-6352 (1-335) x ADF43555 (1-999)		8 AsnAsnSerSerAsnSerSerLysGluSerSerLysAspGly		48 GluGluGlyThrThrLysValProLysHisProLysArgValValValLeuGluTyrSer 6		193 GCCACTGACGTGTGTTTTTAGGTGTTTAAACTGTGTGGGGGGGTGTAGGAGGAGGGGGGGG	10	m	108 ArgLysGlnProAsnLeuGluGluIleSerLysLeuLysProAspLeuIleIleAlaAsp 127	8 ASIASIARGHISLVSGIVILETVILVSASDJenARNIVSIJAAJAPromhrilogius	373 AAAGTTAGAAATGAAAAGTTTACGATCAATTATCTAAAATCGCACCAACAGTT 426	16	427TCTACTGATACAGTTTTCAAATTCAAAGATACAACTTAATGGGGAAAGCT 480	168 LeuGlyLysGluGluGluGlyLysLysArgLeuGluGluHisAspLysLysleGluGlu 187	### ##################################	4	2	589 GCTTCAGTTGTTAACTTCCGTGCTGATCATACAAGAATTTATGCTGGTGGATATGCTGGT 648	LeuSerAspAspValThrLysGlyLeu 24	S GAMALICITAAATGATTTAGGATTCAAACGTAATAAAGACTTA 69		27	751 TTAATGAACGCTGATCATATTTTGTAGTAAAATCAGATCCAAATGCGAAAGGTGCTGCA 810	278 LeuLysGluLeuGluLysAspProValTrpLysLysLeuAsnAla 292	811 TTAGTTAAAAAGACTGAAAGGAATGGACTTCAAGTAAAGAGTGGAAAAATTTAGACGCA 870	293 ValLysAsnGlnArgValAspIleLeuAspArgAspLeuTrpAlaArgSerArgGly 311	871 GITAAAAACAACCAAGTATCTGATGATTTAGAATCACTTGGAACTTAGCTGGCGGA 930	312 LeulleSerSerGluGluMetAlaLysGluLeuValGluLeuSerLysLysAspSerLys 331	931 TATAAATCTTCATTAAAACTTATTGACGATTTATATATGAAAAGTTAAATATTGAA 984
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Novel surface-exposed immunogenic polypeptide of Staphylococcus aureus containing receptors for siderophores or iron-binding ligands, useful for producing antibodies effective against Staphylococci infection.
                                                                                                        Surface-exposed immunogenic polypeptide; SEIP; siderophore; receptor; antibacterial; vaccine; gene; ds.
                                                                                         Staphylococcal surface-exposed immunogenic polypeptide DNA.
                                                                                                                                             Location/Qualifiers
complement(998. .1990)
/*tag= a
/product= "SEIP"
                                                                                                                                                                                                                                              (DSQU-) D-SQUARED BIOTECHNOLOGIES INC.
                                  Claim 4; Page 51-52; 62pp; English.
332 іувАврАвпіув 335
         |||| :::|||
985 AAACAATCAAAA 996
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The present sequence is that of DNA encoding novel Staphylococcus aureus surface-exposed immunogenic polypeptide (SEIP) D2 SA02. To isolate SEIP sense, an expression library of S. aureus genomic DNA was screened with anti-SEIP antisera. DNA was isolated from clones expressing SEIPs, and amino acid sequences were deduced and analysed for conserved and/or functional domains. The SEIP encoded by the present DNA sequence has sequence homology with the sidecrophore family of periplasmic binding production and recovery of SEIPs. The SEIPs can be used individually, or in combination, to produce anti-staphylococcal antibodies useful in staphylococcal infection. They can also be used to develop diagnostic assays

Sequence 2940 BP; 955 A; 514 C; 512 G; 959 T; 0 U; 0 Other;

Alignment Scores:			
Pred. No.:	4.57e-29	Length:	2940
Score:	405.00	Matches:	113
Percent Similarity:	51.74%	Conservative:	65
Best Local Similarity:	32.85%	Mismatches:	132
Query Match:	23.96%	Indels:	34
DB:	8	Gabs:	12

US-10-724-972A-6352 (1-335) x ACC48531 (1-2940)

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8 LeuLysIleLeuSerValIleGlyLeuLeuPheValLeulleAlaThrAlaAlaCygGly 27

Staphylococcus aureus contig SEQ ID #238.

(first entry)

16-MAR-1999

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1246 TIPATGAACGCTGATCATATTTTTGTAGTAAAATCAGAATCCAAATGCGAAAGATGCTGCA 1187
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                                                  1924 GGGAATTCAAATAAACAATCATCTGATAACAAAGATAAGGAAACAACTTCAATTAAACAT 1865
                                                                                                                                             CAAAAACCGAAATTCGAATACATAAAAATGATTTAAAAGATACTAAGATTGTAGGTCAA 1685
1978 AITAAAATGCTT----GTTGTTACGCTTGCTTTCCTACTTGTT----TTAGCAGGATGTAGT 1925
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This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM, Homology searches using content of the Staureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are contined in a vaccine composition against Staureus infection. The be used in a vaccine composition against Staureus infection of collypeptides can also be used in a kit for the immunodetection of collypeptides can also be used in a kit for the immunodetection of including cellulitis, eyelid infections, food poisoning, osteonyelitis, syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences can be used for their fragments) are useful as primers or probes for isolating chandle medium
                                                                                                                                                                                                                                                                                                                                                                                                            /note= "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"
                                                                                                                                                                                                                                                                                            /*tag= a //heae bases represent a line of missing text in /note= "these quence listing in the specification. They are the sequence listing in the nucleotide numbering given in the specification for this DNA sequence" 33420
                                                                                                                 Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polynucleotide(s) and proteins derived from Staphylococcus aureus -stored on computer readable medium and used in the production of anti-S.aureus vaccines.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dillon PJ, Fannon MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 1021-1023; 3271pp; English.
                                                                                                                                                                                                                                                  Location/Qualifiers
1561. .1620
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                                                                                                                                                                                toxic shock syndrome; ds
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                                                                                                                                                                                                                        Staphylococcus aureus.
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3775 113 65

Length: Matches: Conservative:

6.25e-29 405.00 51.74%

Percent Similarity:

AAV74549 standard; DNA; 3775 BP.

AAV74549 ID AAV7

Alignment Scores:

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167
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                                                                                                                                                                                                                                                     88 LysAsnArgIleIleLysProLeuArgAspLysIleGlyLysTyrThrServalGlyThr 107
                                                                                                                                                                                                                                                                         295 CAAAAACCGAAATTCGAATACATAAAAAATGATTTAAAAGATACTAAGGTTCTAGGTCAA 354
                                                                                                                                                                                                                                                                                                 108 ArglysGlnProAsnLeuGluGlulleSerLysLeuLysProAspLeulleIleAlaAsp 127
                                                                                                                                                                                                                                                                                                               GAACCTGCACTAAAATTTAGAAAATCTCTAAATTAAAAACCGGACTTAATTGTCGCGTCA 414
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                                                                                                                AsnAsnSerSerAsnSerSerLysGluSerSerLysAspGlyValGluIleLysHis
                                                                                                                                     115 GGGAATTCAAATAAACAATCATCIGATAACAAAGATAAGGAAACAACTTCAATTAAACAT
                                                                                                                                                           48 GluGluGlyThrThrLysValProLysHisProLysArgValValLeuGluTyrSer
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34
12
  Mismatches:
Indels:
Gaps:
                                              (1-3775)
                                           US-10-724-972A-6352 (1-335) x AAV74549
32.85% 23.96%
Best Local Similarity:
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WPI; 2003-029926/02. P-PSDB; ABU17675.

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Zyskind JW;
Xu HH;
                                                                              Antisense; ds; prokaryotic essential gene; cell proliferation;
                                                                                                                                                                                            Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                            Haselbeck R,
Yamamoto R,
                                                                     gene #3202
                                  BP.
                                                                                                                                                                                           Zamudio C, Malone C,
Trawick JD, Carr GJ,
                                                                                                                                            21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-00948993.
08-FEB-2002; 2002US-0072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                  21-MAR-2002; 2002WO-US009107
                                  ACA21545 standard; DNA; 972
       1027 AAACAATCAAAA 1038
                                                        (first entry)
 LysAspAsnLys 335
                                                                                                                                                                               (ELIT-) ELITRA PHARM INC.
                                                                    Prokaryotic essential
                                                                                                Bacillus anthracis
                                                                                     drug design; gene.
                                                                                                           WO200277183-A2.
                                                        19-JUN-2003
                                                                                                                      03-OCT-2002
                                             ACA21545;
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                      RESULT
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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (3) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibited by the contisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibited by the antisense nucleic acid; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation or the biological pathway in which a proliferation, or that inhibits proliferation of an compound activity against a proliferation of an proliferation that inhibits proliferation of the strains is present in a culture or collection of the strains; or (13) identifying the target of a compound that inhibits the cross or dentifying the target of a compound that inhibits the collection of an organism. The antisense nucleic acids are useful for strains; or (13) identifying the target of a compound that inhibits the collidar proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids are useful collidar proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs. Claim 14; SEQ ID NO 9415; 1766pp; English.

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LeuleualaHisProSerasnSerTyrValGlyGlnPheLeuSerGlnLeuGlyPheLys 229
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ATTGCACCAACAGTTATGTTTGATCCATCAACAAGCAATAACGATCACTTTGCTGAAATG 462
                                                                                                                                                                                                                                                                                                                                                     AspAsnLysLysAsnArgIleIle------LysProLeuArgAspLysIleGly 100
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                                                                                                                                                                                                                                                                                                           GluTyrSerPheValAspAlaLeuValAlaLeuAspValLysProValGlyIleAlaAsp 84
prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                      54
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                                                     U; 0 Other;
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1116
159
122
13
                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                       BP; 405 A; 147 C; 183 G; 237 T; 0
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391.00
51.93*
34.42*
23.14*
                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                          Sequence 972
                                                                                gnment Scores:
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The invention describes a method of monitoring differential expression of capers in a first Bacillus cells relative to expression of the genes in other Bacillus cells, comprising hybridising labelled nucleic acid probes soluted from Bacillus cells to a substrate containing array of Bacillus containing sequenced tags (GST), examining the array, and determining capens in a first Bacillus cells relative to expression of a spot in the array. The method is useful for measuring the expression of cannot be more second Bacillus cells. The method is useful for monitoring new containing the expression of several genes from a Bacillus cell, discovering new genes, identifying possible functions of unknown open reading frames and capens, identifying possible functions of unknown open reading changes in expression of genes may be used to provide a representation of the way in white Bacillus cells adapt to changes in culture conditions.

Convictoring gene copy number variation and stability. Monitoring changes in environmental stress or other physiological provocation. Extensive follow cup characterisation is unnecessary, when one spot on an array equals one correct expresents a genomic sequence information is available.

Continued the printed specification, but was obtained in electronic format correctly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                       308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Monitoring differential expression of several genes in first Bacillus cell relative to expression of same genes in one or more second Bacillus cells, by using substrate containing Bacillus genomic sequenced tag
                           :::|||
850 GAATTAAAGTTTAAAAAAAAAAAAAAATGTATAAATTAAAATAAAAGGCGACACTTGGATTTTC
AsnlysAlaSerSerAsnGluProSerLeuLysGluLeuGluLysAspProValTrpLys
                                                                         289 LysieuAsnAlaValiysAsnGlnArgValAspIleLeuAspArgAspLeuTrpAlaArg
                                                                                                                                                 309 SerArgGlyLeulleSerSerGluGluMetAlaLysGluLeuValGluLeu 325
                                                                                                                                                                         tag; GST;
                                                                                                                                                                                                                                                                                                                                                                                                                  Differential gene expression; genomic sequenced altered culture condition; environmental stress; physiological provocation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; SEQ ID NO 2061; 200pp; English.
                                                                                                                                                                                                                                                                                                                                                                                       Bacillus licheniformis genomic sequence
                                                                                                                                                                                                                                                                        BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NOVO ) NOVOZYMES BIOTECH INC. (NOVO ) NOVOZYMES AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-OCT-2000; 2000US-00680598.
27-MAR-2001; 2001US-0279526P.
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                                                                                                                                                                                                                                                                      ABK74770 standard; DNA; 944
                                                                                                                                                                                                                                                                                                                                                13-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus licheniformis.
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain creaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed control of (II) is useful in gene therapy techniques to restore normal activity of (II) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food of sites expressing (II). (I) and (II) are useful in medical imaging of supplement. (II) and (II) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or bological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations of and to produce other types of data and products dependent on DNA and cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and confine sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in the print of the product of produce of the invention are sequences.
Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss.
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping.

CC and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed conditions as expressed sequence tags for identifying expressed conditions as expressed sequence tags for identifying expressed conditions as expressed sequence tags for identifying expressed conditions as expressed sequences, responsible in gene therapy techniques to restore normal consistent of the protein expression or biological in medical imaging of supplement. (II) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of polypeptide and polynucleotide sequences have applications in consisting and to produce other types of data and products dependent on DNA and cannot be produce other types of data and products dependent on DNA and conditions expensions for the invention. Note: The sequence data for this conding sequences of the invention. Note: The sequence data for this expension of mutations conditions and approar in the printed specification, but was obtained in expension of mutations.
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LeuAsnalaValLysAsnGlnArgValAspIleLeuAspArgAspLeuTrpAlaArgSer 309
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         145 IleGluLeuLysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThrile
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the sequence listing in the specification. They are included to maintain the nucleotide numbering given the specification for this DNA sequence"
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This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can composition against S.aureus infection. The polypeptides can also be used in a kit for the immundetection of S.aureus in a sample. S.aureus is food poisoning, osteomyelitis, shouly including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scaleds skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences can be used can their fragments) are useful as primers or probes for isolating changes can be medium and augical mand and surgines are negetual so primers or probes for isolating changes can be medium chair fragments).
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stored on computer readable medium and used in the production of anti-
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                                                                                                                                                                                                                                                            Ω,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 1239-1240; 3271pp; English.
                                                                                                                                                                                                                                                        Dillon
                                                                                                                                                                                                                                                            Barash SC,
    97EP-00100117.
                                                                                  96US-0009861P.
                                                                                                                                                                         SCI INC.
                                                                                                                                                                 (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                   Choi GH,
                                                                                                                                                                                                                                                                                                                                      WPI; 1997-374922/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .aureus vaccines.
07-JAN-1997;
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U; 60 Other; T; G; 190 Sequence 668 BP; 216 A; 83 C; 119

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                                                                                                       210 LeuLeuAlaHisProSerAsnSerTyrValGlyGlnPheLeuSerGlnLeuGlyPheLys
                                                                                                                      250 GlnMetAsnThrGluThrLeuSerGlnValAsnProGluArgMetPheIleMetThrAsn
                                                                                                                                                                                                                    230 GluAlaLeuSerAspAspValThrLysGlyLeuSerLysTyrLeuLysGlyProTyrLeu
                                                                                                                                                                                                                                                  270 LysAlaSerSerAsnGluProSerLeuLysGluLeuGluLysAspProValTrpLysLys
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Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                              US-10-724-972A-6352 (1-335) x AAV74666 (1-668)
         355.00
70.49%
58.20%
21.01%
                  Percent Similarity:
Best Local Similarity:
Query Match:
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain sequences. (I) is useful as hybridisation probes, polymerase chain caraction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of control of the control of control of the control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of contr
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TIGAAIGCAGTIAAAAAIAAICGCGIGGAIAIIGITIGACCGIGAIGITIGGGCAAGAICT 301
                                                    ArgGlyLeuIleSerSerGluGluMetAlaLygGluLeuValGluLeuSerLygLygABPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     novel human diagnostic protein #13139.
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                                                                                                                                                                                                                                                                                                  AAS77335 standard; cDNA; 2799 BP.
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23-AUG-2000; 2000US-00649167
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Alignment Scores

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                                                                                                                                                                                                                                                                                                                             145 IleGluLeuLysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThrile 164
                                                                                                                                                                                                                                                                                                                                                                        165 SerLysAlaLeuGlyLysGluGluGluGlyLysLysArgLeuGluGluHisAspLysLys 184
                                                                                                                                                                                        85 AspasniyslyshsnargllellelysProLeuargAspLyslleGlyLysTyrThrSer 104
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                                                                                                   45 IleLysHisGluGluGlyThrThrLysValProLysHisProLysArgValValLeu
                                                                                                                                               GluTyrSerPheValAspAlaLeuValAlaLeuAspValLysProValGlylleAlaAsp
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             Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
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AGENCOURT Shultzomi

Mus muscr

GR Eb013 ENTFKS1TF Tetraodon

BW253010 BW254793

AL854856 BW222839 BW235942 Mus muscu CR426562

Tetraodon

603167626

BW248137 BW441129 BW055754

Tetraodon BJ706325

AL666132 BJ712865 BJ707678

Perfect score:

Run on:

Scoring table: Sequence:

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CL694436 10-JUL-2004 PRI0164b.BR (776) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic
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Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.
AppaDB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
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Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601498
Exa: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
Seq primer: T7
Class: fosmid ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazca; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridas; Pristionchus.
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BI4005625
AY4205625
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CR673121 1
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/mol_type="genomic DNA"
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BW48137
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AUTHORS
TITLE
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CL674627 PRI0112c_
CR307287 HDA1--06-
BE422885 EST399330
CL682049 PRI0132d
ALIS1412 Anopheles
CL65859 PRI0144 G
CL665859 PRI0152b_
CL666398 PRI0152b_
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3303.505 Million cell updates/sec
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                      version 5.1.6
- 2005 Compugen Ltd.
                                                                                                            OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34239544 seqs, 19032134700 residues
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CL665859
CL666398
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Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Copyright (c) 1993
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9b_htc::*

9b_est3:**

9b_est5:***

9b_est6:***

9b_gs81:**
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P. pacificus
                                                                                                                                           1 (bases 1 to 801)
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.
Appadbs an Aceds database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
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Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Eas: 00497071601439
Email: ralf. sommerætuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
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/mol type="genomic DNA"
/strain="California"
                                                                                                             Eukaryota; Metazoa; Nematoda; Chr
Neodiplogasteridae; Pristionchus.
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                                                CL674627.1 GI:50177972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167 AlaLeuGlyLysGluGluGluGlyDyBlysArgLeuGluGluHisAspLysLysIleGlu 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187 GluTyrLysLysGluIleThrMetAspLysAsnGlnLysValLeuProAlaValAlaAla 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 ProTyrLeu---GlnMetAsnThrGluThrLeuSerGlnValAsnProGluArgMetPhe 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    211 GITGCCCACTATCGC-----GAAGAGCATTGTTAAACGCTGGCAACAAGATCCG 161
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/strain="california"
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/clone_llb="Mixed stage fosmid library of P. pacificus
var. California"
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                                                                                                                                                                                                                                                                                                GATGCAAAACGCATCCTGCCCGAAGTGCGTGCGCACCTGAAACCGTGGCAGTCCGTCGGA
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                                                                /note="Vector: pEpifos-5 Fosmid vector"
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531 bp mRNA linear EST 18-MAY-2001 fruit, TIGR Lycopersicon esculentum cDNA
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Alcala, J., Vrebalov, J., White, R., van der Hoeven, R.S., Holt, I.E., Liang, F., Hansen, T.S., Craven, M.B., Bowman, C.L., Ronning, C.M., Marman, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and Tanksley, S.D.
Generation of ESTs from tomato fruit tissue, breaker stage
                                                                                                                                                                                                                                                 GGCGAAATGGTGGGTAAAAAGGGGAGATGCAGGCACGTCTGGAACAACATAAAGAGAGG 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     199 ATGGGGCAGTGGGCCAGCCAG ----CTTCCCAAAGGACACGCGTGGCCTTTGGCACA 146
                                                                                                                                                             GITCAGGACGAACAGGCACGITIACCTCGAAAAACGCCACAACGGATTGTGGTGCTG 560
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100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
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Conservative:
Mismatches:
Indels:
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/db xref="taxon:39947"
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/tlssue type="callus"
/dev stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="s.coli SoLi"
/lab_host="s.coli SoLi"
/lab_host="s.coli SoLi"
/clone lib="OsHDAC1-overexpressing transgenic rice lambda phage cDNA library I (HDA1)"
/clone lib="WetCor: pBluescript SK(+); Site 1: EcoRI; Site 2: Note="WetCor: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Callus was treated with ABA(20um) for lhour. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."
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SM Oryza sativa (japonica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.

E 1 (bases 1 to 625)

S Kim,J.S., Jun,K.M., Cheong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTS

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193

Fax: 82 31 321 6155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HDA1--06-E11.g1 OsHDAC1-overexpressing transgenic rice lambda phage cDNA library I (HDA1) Oryza sativa (japonica cultivar-group) cDNA CElone HDA1--06-E11, mRNA sequence.
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                                                                                                                                                                                                                                                                    245 LysGlyProTyrLeu---GlnMetAsnThrGluThrLeuSerGlnValAsnProGluArg 263
                                                                                                                                                                                                                                                                                                                                                     MetPhelleMetThrAsnLysAlaSerSerAsnGluProSerLeuLysGluLeuGluLys 283
                                                                                                  205 AlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPheLeuSer 224
                                                                                                                                                                                                                                                                                                                                                                                           703 CTGCTGGTTGCCCACTATCGC-----GAAGAGAGCATTGTTAAACGCTGGCAACAA 753
                                            :::
:-----AACGTTCCCGCTGCGATG
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                                                                                                                                          553 TCACGCGAACAGCAATTCAACCTGCATACTCAGGAGACCTGGACCGGCAGCGTGCTGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                    AspProValTrpLysLeuAsnAlaValLysAsnGlnArgVal 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---ValAsnProGluArgMetPheIleMetThrAsnLysAlaSerSerAsnGluProSer 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LeuLysGluLeuGluLysAspProValTrpLysLysLeuAsnAlaValLysAsnGlnArg 297
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                                                                                                                                                                         /db_xref="taxon:54126"
/clone lib="Mixed stage fosmid library
var. California"
/note="Vector: pEpifos-5 Fosmid vector"
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                                                              /organism="Pristionchus
/mol type="genomic DNA"
                                                                                                          /mol_type="genomic D|
/strain="California"
   Location/Qualifiers
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152.00
42.91%
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Pristionchus pacificus
Pristionchus pacificus
Bristionchus pacificus
Butaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridas; Pristionchus.

I (bases 1 to 760)
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.
AppaDB: an Aceda Raes. 32 (1), D421-D422 (2004)
Pristionchus pacificus
Nucleic Acids Raes. 32 (1), D421-D422 (2004)
Evolutionary Biology
Max-Planck-Trastitute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 0049707160149
Email: raif:sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seg primer: T7
Class: fosmid ends.
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Conservative:
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OBJECTO01947 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.
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Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota; Vizidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Epermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 2019)
Ma.L., Wangc, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M., Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L., Mong, G.K.S., Deng, X.W. and Wang, J.
An analysis of transcriptional regulation of the rice genome and unpublished (2004)
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                                                                                            148 sSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThrIleSerLysAlaLe 168
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                                                                                                                                                                                                                                                         188 rLysLysGlulleThrMetAspLys-----AsnGlnLysValLeuProAlaValAl
                                                                                                                                                                                                                                                                                                                                     aAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPheLeuSerGl
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Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
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                                                                                                               CNS01MUR Seambiae GSS T7 end of clone 22J04 of NotreDamel library from strain PEST of Anopheles gambiae (African malaria mosquito),
                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage :
Br 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
2 (bases 1 to 966)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 GlulleLysHisGluGluGlyThrThrLysValProLysHisProLysArgValValVal 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 LeuGluTyrSerPheValAspAlaLeuValAlaLeuAspValLysProValGly-IleAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr. Soux, Paris 75015, France
This clone is from an A. gambiae BAC library provided by F.H. Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut
                                                                                                                                                                                                                                                     Anopheles gambiae (African malaría mosquito)
Anopheles gambiae
Eukaryota: Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Roth, C.W., Brey, P.T., Ke, Z., Collins, F.H. and Weissenbach, J. Direct Submission
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Conservative:
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                                                                                                                                                                        genomic survey sequence.
AL151412
AL151412.1 GI:7011891
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PRIO14d_G07 - PRIO14d,B21 (810 bp DNA linear GSS 09-JUL-2004 parificus var. California Pristionchus pacificus genomic, genomic survey sequence.
-AATGAGTTGCTGCGTCTCGCAATT 1953
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:54126"
/clone_lb="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"
                                                                                                                                                                                                                                                                                                              Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J. AppaDB: an AcedB database for the nematode satellite organism Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RB:
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                                                                                                                                                                                                                                       Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: ralf.gommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and
sequenced at Vancouver, Canada.
                                                                                                                                                                                                                                                                                                                                                                                         Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannatr. 37-39, Tuebingen D-72076, Germany
Fax: 00497071601371
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1 (bases 1 to 810)
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/organism="Pristionchus
/mol_type="genomic DNA"
/strain="California"
                                                                  1954 GCTGAGGCACAGGAAAAGAATAAG 1977
                                              328 LysAspSerLysLysAspAsnLys 335
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                                                                                                                                                                                                                                          ---ValAsp 70
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Mismatches:
Indels:
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                                                                                                                                                  (1-335) x CL958706 (1-2019)
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                                                          126.50
39.33%
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A137 bp DNA linear GSS 12-DEC-2003
Homo sapiens HCM7097 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockwille, MD 20850, USA
This sequence as made by sequencing genomic exons and ordering them based on alignment.
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                   LysLysAsnArgileileLysProLeuArgAspLysileGlyLysTyrThrSerValGly 106
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1 (Dases 1 to 4137)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Tanenbaum, D.M., Civello, B., Ferritera, S., Mang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone lib="Mixed stage fosmid library of P. pacificus var. California" /note="Vector: pEpifos-5 Fosmid vector"
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Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.
AppaDB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
                       end
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Neodiplogasteridae; Pristionchus.
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Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and
sequenced at Vancouver, Canada.
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                                                                        312 LeulleSerSerGluGluMetAlaLysGluLeuValGluLeu 325
                                                                                                296 ATTTTTGCTGCAGAGCGTATTGCCGCTGACACGGTAAAATC 337
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Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
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/mol_type="genomic DNA"
/strain="California"
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Pristionchus pacificus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="Aggregation stage"
/clone_lib="Dictyostelium discoideum cDNA library, AF"
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334 Gaaaagaaaattatgaaaaatcaaatta
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/clone="dda27b21"
1111 Yata, Mishima, Shizuoka 4
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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                                                                                                                      /mol_type="mRNA"
/strain="AX4"
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        3076 AAAACAGACGAGCTAAACAAACAGTTAAAAGACTTGTCACAGAAATACACGGAAGTAAAG
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                                       107 ThrarglysGlnProAsnLeuGluGluIleSerLysLeuLysProAspLeuIleIleAla 126
                                                                                                                                                                    LeuAsnLyslleAlaProThrIle-----GluLeuLysSerPheAspGlyAspTyrAsn 155
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Dictyostelium discoideum
Dictyostelium discoideum
Bukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases I to 764)
Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
Full length cDNA of Dictyostelium discoideum at the aggregation
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                                                           AATGTGAAAGAGGAAGTAGTAGAAGAAAATGCCAAAACAGACTTCTGAGATACTTGCAGTG
                                                                                                       127 AspAsn-----AsnArgHis--------LysGlyIleTyrLysAsp
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Conteat: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
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Bukaryota, Entamoebidae; Entamoeba.
Bukaryota, Entamoebidae; Entamoeba.
Bukaryota, Entamoebidae; Entamoeba.
Bukaryota, Entamoebidae; Entamoeba.
Bukaryota, Van Aken, S. and Fraser, C.
Deftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica numbished (2000)
Contect: Brendan J Loftus
Contect: Brendan J Loftus
Contect: Brendan J Loftus
Contect: Brendan J Loftus
The Institute for Genomics
The Institute for Genomic Research
Fil. 301 801 80208
Fax: 301 808 8038
Fax: 301 808 8038
Fax: 301 808 8038
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                                                                                                                 LeuLysProAspLeullelleAlaAspAsnAsnArgHisLysGlyIleTyrLysAspLeu 138
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                                                  139 AsnLysile-----AlaProThrileGluLeuLysSerPheAspGlyAspTyrAsnGlu 156
                                                                                                                                                                                                                                                                                                                                                    -----TTATCTAATGCAGAAAAGAAAACGGCATCTACTTCTAATTTTAAAGAA 486
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                                                                                                                                                               --TACACTGCTAGAAGTAAGAAGTA
                                                                                                                                                                                                                                                      388 CAACAGTTATCAACAAGTACAAAAAAAAAAAAAAAAATTTGATCAAGAC-----
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/db_xref="http://dc.db.
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/dc.db. lb="Entamoeba histolytica at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
                                                                                                                                                                                                                                                                                                                                                                  9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Tel: 301 838 344
Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
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  Entamoeba histolytica Sheared DNA Entamoeba histolytica
                                                                                                                                                        Eukaryota, Entamoebidae, Entamoeba.

1 (bases 1 to 839)
Loftus, Pan Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HM1:IMSS sheared DNA library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SerlysGluSerSerlysAspGlyValGluIleLysHis-----GluGluGlyThrThr
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                                                                                                                                                                                                                                                                           Unpublished (2000)
Conteact: Brendan J Loftus
Department of Bukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-724-972A-6352 (1-335) x AZ532836 (1-839)
                          genomic, genomic survey sequence.
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High quality sequence stop: 820.
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Seg primer: M13-Forward
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CL957361 1782 bp DNA linear GSS 21-SEP-2004 OBIPCCO00458 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.
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Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatrophyta, Magnoliophyta; Liliopsida; Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
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                                                                                                                                                  292 AlavaliyaAsnGinArgValAspIleLeuAspArgAspLeuTrpAlaArgSerArgGly 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 GlyAsnAsnSerSerAsnSerSerLysGluSerSerLysAspGlyValGluIleLys 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47 HisGluGluGlyThrThrLysValProLysHisProLysArgValValValLeuGluTyr 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ma,L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wangc,X., Cao,M., Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L., Wong,G.K.S., Deng,X.W. and Wang,J. An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis
                                                                           272 SerSerAsnGluProSerLeuLysGluLeuGluLysAspProValTrpLysLysLeuAsn
                                       259 GAAGAAGAA-----AGACAAATAGAAGAAGAAGACAA-----ATAGAAGAAAAG
                                                                                                                                                                                                                          312 LeulleSerSerGluGluMetAlaLysGluLeuValGluLeuSerLysLysAspSerLys
                                                                                                                                                                                                                                                          -----CAAGAAAAAAACAACTTAGAAAACTATTAGTAAG
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/note="Oryza sativa exon trapped genomic sequen
                                                                                                  Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
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Fax: 86-10-80488676
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/note="Vector: pHOS1; Site 1: Bat I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102 TyrThrSerValGlyThrArgLysGlnProAsnLeuGluGluIleSerLysLeuLysPro 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142 AlaProThrIleGluLeuLysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPhe 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----LysArgLeuGluGluHisAspLysLysIle---GluGluTyrLysLysGlu 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42 GlyValGluIleLysHisGluGluGluGlyThrThrLysValProLysHisProLysArgVal 61
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High quality sequence start: 13
High quality sequence stop: 814
Location/Qualifiers
                          genomic, genomic survey
BH132864
                                                     BH132864.1 GI:15091925
                                                                              Entamoeba histolytica
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|1318 CTCCAGGAACTCCACGCGGAAATCAAAAGCATCCATTAGCAGTGAGAAGCAGATCTCC 1377
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859 GAAGGTGATCTAGCAAAAATGTCACAAGAAAATTGCAGCTCGAGGCCCAGGTTAAGGAA 918
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                                       98
104 SerValGlyThrArgLysGlnProAsnLeu------GluGluIleSerLysLeu
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919 CTTGAACAAGCATCTCGCAGCCTAGATGATTCATCAGCACAGATTATGAAGCTCCAAGAA
                                                                                          LysLys------AsnArgllelleLysProLeuArgAspLyslleGlyLysTyrThr
                                     SerPheValAspAlaLeuValAlaLeuAspValLysProValGlyIleAlaAspAspAsn
                                                              GAGCTTCAGGAAGGAAAAACTTGAG------GCACTTGAGGAAAAGAAT
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|1096 GTCGCAGAACTACAAGCTACAATCAACAATCTGAAAGCTGAC------
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/ Branl="Mnillands"
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// Clone_lib="Entamoeba histolytica Sheared DNA"
// Clone_lib="Weator: ph051; Site_: Bst !; Constructed at The Institute for Genomic Research (TigR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond, L.S. (Jark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)." 897 bp DNA linear GSS 07-AUG-2001 Entamoeba histolytica Sheared DNA Entamoeba histolytica Email: bjloftusotigr.org Clones are derived from the Entamoeba histolytica HM1:IMSS sheared DNA library Seq primer: M13-Reverse GATGGTATGATATCTTCAAGAAGTATATCAATC-----AAAAAGAAAAAGATA 703 ileLysProLeuArgAspLys1leGlyLysTyrThrSerValGlyThrArgLysGlnPro 111 ------ATACTTAAAAATATGAGGTAAAAGAAAA 751 ThrLysValProLysHisProLysArgValValValLeuGluTyrSerPheValAspAla 71 LeuValAlaLeuAspValLysProValGlyIleAlaAspAspAsnLysLysAsnArgIle 91 Loftus, B., Wang, Z., Van Aken, S. and Fraser, C. Determination of clone end sequences from Entamoeba histolytica HMI:IMSS sheared DNA library (2001) SerAsnSerSerLysGluSerSerLysAspGlyValGluIleLysHisGluGluGlyThr Unpublished (2001)
Context: Brendan J Loftus
Context: Brendan J Loftus
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850,
Fax: 301 838 9308 897 68 57 1114 71 /organism="Entamoeba histolytica" /mol_type="genomic DNA" /strain="HM1:IMSS" Length: Matches: Conservative: Mismatches: Entamoeba histolytica Eukaryota; Entamoebidae; Entamoeba. Indels: US-10-724-972A-6352 (1-335) x BH132864 (1-897) seguence. Gaps: :: 92 ò

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BQ065769 1005 bp mRNA linear EST 02-APR-2002
AGENCOURT 6875095 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5930336
5', mRNA @equence.
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1062 GATTCTGTTGTGGAAGACTTA-----CATTTACAAAATAAATACCTTCAAGAAAAACTT 1115
                                                                                                                                                                                                                                                                   1236 TCTGAAAACATCGAGCTGAATTT---CAACTTGAACAAGCAAATAAAGATTTGCCAAGA 1292
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(Dases 1 to 1005)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Standt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:
http://image.llnl.gov
Plate: LLCM2109 row: o column: 09
High quality sequence stop: 670.
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                                            224 SerGlnLeuGly-----PheLysGluAlaLeuSerAspAspValThrLysGlyLeu
                                                                                       1116 CATACTTTAGAAAAAAACTTTCAAAGGAGAAATATTCTCAGTCTTTGACTTCAGAAATA
                                                                                                                                 241 SerLys-----TyrLeuLysGlyProTyrLeuGlnMetAsnThrGluThrLeuSer
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KELENFDPSFFEEIEDLKYNYKEEVKKNILLEEKLKKLSEQFGFELPSPLAASEHSED
3ESPHSFPIY"
                                                                                    /trānslation="MLQETHASEVKKVKAEVEDLRHALAQAHKDSQSLKSELQAQKEA
NSRAPTTHRNLVDRLKSQLALKEKQQKALSRALLELRSEWTAAAERSI IAVTSQKEA
NLNVQQVVERHTRELKSQI EDİNENLLKLKEALKTSKNKENSLADDLNELNNELQKKQ
KAYNKILREKQGI DÖĞNDELARQIKLSSGLQSKTLIDNKQSI IDELQKKVKKLESQL
ERKVDDVDI KPVKEKSSKEELI RWEEGKKWQTKVEGLRNELKEKEEGAL
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TQQALPRDSVVEDLHLONKYLQEKLHTLEKKLSKEKYSQSLTSRIESDDHCQKEQELQ
KENLKLSSENIELKPQLEQANKDLPRLKNQVKDLKEMCEFLKKGKLELERKLGOVRGA
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KLAHFGROLSMQFESKNKOTEKI VABNERLIKELKEI EASEKLKI JAKNNLELVNDK
MAAQLEETGKRLQPASSRAPQLEGADSKSWKSI VVSR YYETKNKELESDI AKKNQSIT
DLKQLVREATEREQKAKKYTEDLEQQI EI LKNVPEGABTEQELI RELQLLRLANNQMD
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Matches:
Conservative:
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Indels:
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                  /codon_grart=1
/proteIn_id="BAC26700.1"
/db_xref="G1:26325892"
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Sequencing and microarray development
L. Am. J. Respir. Cell Mol. Biol. 30 (3), 296-310 (2004)
Conteat: Shultz MA
Dept. of Molecular Biosciences, School of Veterinary Medicine
University of California, Davis
1311 Haring Hall, One Shields Avenue, Davis, CA 95616, USA
Tel: 530 752 4698
Email: mashultz@ucdavis.edu
Average Phred score is 20 or better. All poor quality data (Phred < 20) and vector/linker sequence has been removed.
High quality sequence stop: 1065.
                                                CF109973 1005 bp mRNA linear EST 23-JUL-2003 Shultzomica03224 Rat lung airway and parenchyma cDNA libraries Rattus norvegicus cDNA clone Contig2841 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="airway or parenchyma"
/dev_stage="adult"
/clone_lib="Rat lung airway and parenchyma cDNA libraries"
/note="Organ: lung; Vector: pGEM-11Zf(-); Site_1: Eco RI;
Site_2: Not I; mRNA was isolated from microdissected rat
lung airways and parenchyma tissues."
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                                                                                                                                                                          Rattus norvegicus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||||||||
413 AACAATGAAGAAGAATCTGCCTCAAAACAAGATAAAAAGAAGAAGAAGAAAAAAAGGCAAG
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Shultz,M.A., Zhang,L., Gu,Y.-Z., Baker,G.L., Fannuchi,M.V.,
Badua,A.M., Gurske,M.A., Morin,D., Penn,S.G., Jovanovich,S.!
Plopper,C.G. and Buckpitt,A.R.
Gene expression analysis in response to lung toxicants: I.
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="Contig2841"
                                                                                                                                                         Rattus norvegicus (Norway rat)
                                                                                      CF109973.1 GI:33165360
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sex="male"
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117.00
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ORGANISM
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AUTHORS
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COMMENT
                  RESULT 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 GlyThrArgLysGlnProAsnLeuGluGluIleSerLysLeuLysProAspLeuIleIle 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 AlaAspAsnAsnArgHisLysGlyIleTyrLysAspLeuAsnLysIleAlaProThrIle 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 GluLeuLysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThrIleSer 165
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                                                                                                                                                                                                                                            HisGlu---GluGlyThrThrLysValProLysHisProLysArgValValValLeuGlu 65
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                                                                                                                                                                          GlyAsnAsnSerSerAsnSerSerLysGluSerSerLysAspGlyValGlulleLys
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61
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                Length:
Matches:
Conservative:
Mismatches:
Indels:
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                0.0265
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us-10-724-972a-6352.rst

Best Local Similarity: 18.96\$ Mismatches: 146 Query Match: 6.92\$ Indels: 103 DB: 9 Gaps: 11	US-10-724-972A-6352 (1-335) x AY407955 (1-5504) Qy 22 AlaThrAlaAlaCysGlyAsnAsnAsnSerSerAsnSerSerLy8GluSerSerLy8Asp 41	Db 4137 GCTGCAGGACTTTGCCAGCACGCAGGAAGACTCTGGAAGAAGAGGAAGAAGAGGTTCCAGAA 4196	Qy 42 Gly-ValGluIleLysHisGluGluGlyThrThrLysValProLysHisPr 58	oLysArgValValValLeuGluTyrSerPheValAspAlaLeuValAlaLeuAspValLy	Db 4257 AAAGACCAAGAACAGGAGCTGGACGACGACGGTTGTTGATTTGGACAACCA 4316 Qy 78 SProValGlyIleAlaAspAsnLy8Ly8AsnArgIleIleLy8ProLeu 95	::::::::::::::::::::::::::::::::::::::	4377 GGAGAAAAACTCTTCCAAATACGCGGATGAGAGGGACAGAGCTGAGGCAGAGGCAGAGCCAGAAGCCAGAAGCCAGAAGCCAGAAGCCAGAAGCCAGAAGCCAAGAAG	Oy 96 gAspLysIleGlyLysTyrThrSerValGlyThrArgLysGlnbroAsnLeuGluGlu1116 	eSerLysLeuLys	126	Db 4557 CAAGGATGACGTCGGGAAGAACGTCCATGAGCTCCAAGCGGCCCTGGAGAC 4616	13.7	4617 CCAGATGGAGGAGATGAAGACGCAGCTGGAAGAGCTGGAGGACGAGCTGCAAGCCACGGA	<pre>QY 13/ pleudsnly81leAlaProIntileGluLeULy8SerFheAspClyAspTyrAsfGluAs 15/</pre>	Qy 157 nIleAspAlaPheLysThrIleSerLysAlaLeuGlyLysGluGluGluGlyLysLysAr 177 :::: :::: ::::::::::::::	177 gLeuGluGluHisAspLysLysLleGluGluTyrLysLysGluIleThrMetAspLysAs	Db 4770 GAGGAGCAACTGCAGAGACAGCTTCACGAGTATGAGACGGAÀGTGGAAGACGAGAAA 4829 Qy 197 nGlnlygValleuProAlaValAlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSe 217	4830 GCAACGTCCCTGCAGCTCCAGCAAAGAAG	217 rTyrValGlyGlnPheLeuSerGlnLeuGlyPheLysGluAlaLeuSerAspAspValTh	DB 4861AMGCIGGAAGGGGGACCIGGAGGCIGGGGCCGGCGCGCTTCAGGCCGTCTGCCAT 4910 Qy 237 rLysGlyLeuSerLysflyrLeuLysGlyProTyrLeuGlnMetAsn 252	 4911 CAAGGGAGGAAGCCATCAAGCAGCTACGCAAACTGCAGGCTCAGATGAAGGACTT	-ThrGluThrLeuSerGlnValAsnProGluArgMetPheIleMetThrAsnLysAlase	DD 4971 ILMANGAGGIGGAAGAIGCCCGIGCCTCCAGAGAIGAGAICTITGCCACAGCCAA 5027 Qy 272 rSerAsnGluProSerLeuLysGluLeuGluLysAspProValTrpLysLysLeuAsnAl 292
Qy 94 ProLeuArgAspLys1leGlyLysTyrThrSerValGlyThrArgLysGlnProAsnLeu 113 Db 602TCTAAAAAAGGTAAAAAAGCCCAGAAATCAACTAAAAAAAA	Qy 114 GluGluIleSerLysLeuLysProAspLeuIleIleAlaAspAsnArg 130	Ογ 130 130	Db 686 GAACGITCGAGAGTAAACTCCTCAGGTGAAAGTGGTGGGGGTCTGATGAATTTTGCAG 745 QY 131HisLygGlylleTyrLygABpLeuAsnLysIleAlaProThrileGluLeuLys 148	Db 746 TCCAGAAAAGGACAGAAAAAATCAGAAGAACAAGTCAGTTCCTACCATAGACAGGGG 805	Oy 149 SerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThrIleSerLys 166 :::	rgLeuG 	187 GluTyrLysLysGluIleThrMetAspLysAsnGlnLys 199	DD 914 AAGGTGAAAGAAAGAGCTAGAQAAGGCCAGGAAG 952 RESULT 19	AY407955 LOCUS AY407955 DEFINITION Home sapiens MYH11 gene, VIRTUAL TRANSCRIPT, partial sequence,	ACCESSION A7407955.1 GI:39763926	_	асмадааа	AUTHORS 1 Cases 1 to 5504) AUTHORS 7 AUTHOR 7 AU	Perriera,S., Mang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargjil,M. TITE Tofering contoured contoured to the persistence of the	¥ 8			JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, ROCKYIILe, ND 20850, USA COMMENT This conjusts are made by seminaring conjusts and and and and and and and and and and	them based on alignment. Location/Qualifiers	1.3504 Organism="Homo sapiens" mol_type="genomic DNA"	/db_xref="taxon:9606" 	/Jocus_tag="HCM3063"	Alignment Scores: Pred. No.: Core: Score: 117.00 Matches: Percent Similarity: 35.32% Conservative: 63

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BJ714899 BF01FFA CDNA Oryzias latipes CDNA clone MF01FFA033h02 5', mRNA sequence.
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                                                            -----TyrThrSerValGlyThrArgLysGlnProAsnLeuGlu 114
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                                                                                                                                                                                        38 SerSerLysAspGlyValGluIleLysHisGluGluGlyThrThrLysValProLysHis
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                                     ArgGlyLeuLys1leLeuSerValIleGlyLeuLeuPheValLeu
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US-10-724-972A-6352 (1-335) x CO573945 (1-804)
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/db_xref="maxon:10116"
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/lab_host="DH10B TonA"
/clone lib="Will MGC 246"
/note="Corgan: llver; Vector: pExpress-1; Site_1: EccRV;
Site_2: Not!; RNA obtained from testist tissue of 8 wk old animal. Tissues were snap-frozen and kept at -80C before animal. Tissues were snap-frozen and kept at -80C before RNA extraction and purification (Tri-reagent method). cDNA was primed using oligo-dT primer:
S'-pGACTAGTTCTAGATGGGAGGGCGCCC(7)25-3' and cloned into the EccRV/Not! sites of pExpress-1. Size-selection >1.25kb resulted in an average insert size of 1.7 kb. This a primary library (normalized library is NIH MGC 247) and was constructed by Open Biosystems. Note: this is a NIH MGC library.
                                                                                                                                                                                                                                                       CO573945
AGENCOURT 28537271 NIH MGC 246 Rattus norvegicus cDNA clone
IMAGE:7272914 5', mRNA sequence.
                                                                                                Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genemics
National Cancer Genemics
National Cancer Institute / NIH
Bldg. 31 Rml0A07 Betheada, MD 20892
Email: cgapbs-r@mail.nih.gov
Tisaue Procurement: Drs. Josef Lazar & Howard Jacob, Medical
College of Wisconsin
CDNA Library Preparation: Open Biosystems
CDNA Library Preparation: Open Biosystems
CDNA Library Preparation: Open Biosystems
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM15519 row: f column: 16
High quality sequence stop: 541.
 292 aValLysAsnGlnArgValAspIleLeuAspArgAspLeuTrpAlaArgSerArgGlyLe 312
                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalla, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/organism="Rattus norvegicus"
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Rattus norvegicus
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                                     5088 CGCCGCCGCTGAGAGG---
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5181 CCAGGACGAGAAG 5193
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei, Acanthomorpha, Acanthopterygii, Percomorpha, Atherinomorpha, Beloniformes, Adrianichthyidae, Oryzinae, Oryzias.

1 (bases 1 to 832)
Mohara,Y., Shin-i,T., Kimura,T., Narita,T., Jindo,T. and Takeda,H. Medaka EST Project in Takeda's lab
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LysGlnProAsnLeuGluGluIleSerLysLeuLysProAspLeuIleIleAlaAspAsn 128
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65
45
91
67
                                                                                           Contact: Tadasu Shin-i
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
Tal: Nata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
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                                                                                                                                                                                                          organism="Oryzias latipes"
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/strain="Hd-rR"
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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes 20499374
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full-length
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases I to 1545)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                           242 LysTyrLeuLysGlyProTyrLeuGlnMetAsnThrGluThrLeuSerGlnValAsnPro
                                                                                                                                                                                    262 GluargMetPheIleMetThrAsnLysAlaSerSerAsnGluProSerLeuLysGluLeu
LeuSerGlnLeuGlyPheLygGluAlaLeuSerAgpAgpValThrLygGly---LeuSer
                                                                                                                                                                                                                                                                                                          AACCAG------ACTGCCGAAAGAGATGAGTACGAGCACCAACAGAAGGAGCTT
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Nature 409, 685-690 (2001)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               291 ---AsnAlaValLysAsnGlnArg 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           809 AGGAATGCCANAGGGAATGCTAGG 832
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Mus musculus (house mouse)
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CO113362 816 bp mRNA linear EST 16-JUN-2004
GR_Eb013122.r GR_Eb Gossypium raimondii cDNA clone GR_Eb013122
3', mRNA sequence.
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Gossypium raimondii
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
1 (bases 1 to 816)
Kim,H., Yu,Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,C.,
Udall,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167 AlaLeuGlyLysGluGluGluGlyLysLysArg---LeuGluGluHisAspLysLysIle 185
                                                                                                                                                                                                                                                                                                                               226 LeuGlyPhelysGluAlaLeuSerAspAspValThrlysGlyLeuSerLysTyrLeuLys 245
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                                                                                                                                                                                                      577 AGCCAGCTTCAGCAGCTGCTGGAGAATCAGAAGAACTCCTCGGTGACCCTGGCGGACACC 636
                                                                                                                                                                                                                                              206 AlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPheLeuSerGln 225
                                                                                                                                                                                                                                                                                                                                                                                                                246 GlyProTyrLeuGlnMetAsnThrGluThrLeuSerGlnValAsnProGluArgMetPhe 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     796 GTCGTCGACATGTCGAAGTACAAAGCCACAAGAACGACTTGGAGACCCAGATTTCCAAC 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               295 ---AsnGlnArgValAspIleLeuAspArgAspLeuTrpAlaArgSerArgGlyLeuIle 313
  147 LeulysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThrIleSerLys 166
                                                                                                                                                                                                                                                                                       637 CTGAAG------CTAAAGGAAGCCCTCGAGAAAGAGGTTGGGATCATGAAAGCCAGC 687
                         -----GAGGAGCTGAGGAGTAAGCAGAGGTGTCTGGAGCGCGAGCAGCAGACGGTG
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Global assembly of Cotton ESTs
Global assembly of Cotton ESTs
Global assembly of Cotton ESTs
Contact: Rod A. Wing
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ, 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu
Plate: 013 row: I column: 22.
Location/Qualifiers
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/dev_stage="11 days embryo"
                                                                                                                                                                                                                                                                    Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Please visit our web site (http://genome.gsc.riken.jp/) for further
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Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Haraka, Hayatseu, M., Hiramoto, K., Hiracka, T., Hori, F., Inotani, K., Ishi, Y., Itoh, M., Izawa, M., Kasukawa, T., Hori, F., Imotani, K., Ishi, Y., Itoh, M., Izawa, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Yoshino, M., Muzamatsu, M. and Hayashizaki, Y., Yoshida, K., Yoshino, M., Muzamatsu, M. and Hayashizaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="similar to UVEAL AUTOANTIGEN [Homo sapiens] (SPTR|Q9BZF9, evidence: FASTY, 79%ID, 32.3%length, match=1353)"
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40
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Conservative:
Mismatches:
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"mol type="mRNA"
'strain="C57BL/6J"
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294

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/db xref="taxon:5759"
/db xref="taxon:5759"
/clone lib="Entamoeba histolytica Sheared DNA"
/clone lib="Wetcor: pHOS1; Site_1: BRI J; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Ilark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Entanoba instolytical Entamoeba.

Eutaryota; Entamoebidae; Entamoeba.

Eutaryota; Entamoebidae; Entamoeba.

Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica HM1:IMSS sheared DMA library

Unpublished (2000)

Loftus
Conteat: Breadan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3543
Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
DMA library
Seq primer: M13-Forward
Class: shottun
                                                                                                                                                                                                                                                                                               889 bp DNA linear GSS 14-NOV-2000
Entamoeba histolytica Sheared DNA Entamoeba histolytica
       GlyLeulleSerSerGluGluMetAlaLy8GluLeuValGluLeuSerLy8Ly8AspSer 330
                                                                                                AsnLysLysAsnArgIleIleLysProLeuArgAsp-----LysIleGlyLysTyrThr 103
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63
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Matches:
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ENTFK51TF Entamoeba histolytica S
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AZ549761
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High quality sequence stop: 852.
Location/Qualifiers
       ||| ::::::
GAAGAGGAAAGAAAGAAAG-
                                                                                                                                                                                                                                                                                                                                                                                      A2549761.1 GI:11174477
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                                                                                                                                                                                                        AAGAACGAGAAGAAG 789
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                                                                                                                                                                                                                                                  RESULT 24
AZ549761
                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
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TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :::||||:::
58 AAGAAAGAAAAGAAGAAGGATGAGGTAGAAGAAGCTGAAGAATTAGAAGGGGGAAAG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----LysProAspLeullelleAlaAspAsnAsnArgHisLysGlyIleTyrLys 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 AAAGAAAAGAAGAAAAGACAAAGAGCGAAGGAGAATAAGAAAAAAA-------AAG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       169 AAGAAGGATGAGGTAGAAGAAGATGAAGAATTAGAAGAGGGAAAGGAAAGAAAGAAAGAAAA 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -------LysSerPheAspGlyAspTyrAsn 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GluAsnIleAspAlaPheLysThrIleSerLys------AlaLeuGlyLysGlu 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     172 GluGluGlyLysLysArgLeuGlu---GluHisAspLysLysIleGluGluTyrLysLys 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GluIleThrMetAspLysAsnGlnLysValLeuProAlaValAlaAlaLysSerGlyLeu 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          231 AlaLeuSerAspAspValThrLysGlyLeuSerLysTyrLeuLysGlyProTyrLeuGln 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         251 MetAsnThrGluThrLeuSerGlnValAsnProGluArgMetPheIleMetThrAsnLys 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                568 GAAGAAGCTGAAGAATTAGAAGAGGGAAATAAAGAAAAGAAGAAGAAAGACAAAGGGGCAAAG 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             271 AlaSerSerAsnGluProSerLeuLysGluLeuGluLysAspProValTrpLysLysLeu 290
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Wendle lab. Directional choned into Not1-EV. Colonies
plated/picked by AGI. More glycerol clones held in -80."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104 SerValGlyThrArgLysGlnProAsnLeuGluGluIleSerLysLeu------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        469 GTAGAAGAAGCTGAAGAA------TAAGAAGAGAGAGAATAAAGAA
                                                                                                                                                                                                                                                                                                                                            816
68
40
119
58
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Matches:
Conservative:
Mismatches:
Indels:
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|1048 GATGACAAGCAGAAGATTTTGGACAAGTGCAACAGGGTCACCATGGCTGGACAAGAAT 1107
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(E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
More information available at
http://www.genoscope.cns.fr/tetraodon.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 GlnProAsnLeuGluGluIleSerLysLeuLysProAspLeuIleIleAlaAspAsnAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         805 GGCATCATGAACGTGTCTGCC-----GTGGACAAAAGCACATGGCAAAGAAAACAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1108 CAG------ACTGCCGAGAAGGACGAGTACGAGCATCAGCAGAAGGAGCTGGAG
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62
50
88
70
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Matches:
Conservative:
Mismatches:
Indels:
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(CR650378.1 GI:51146823

S HTC; CDNA; full-length; Tetraodon nigroviridis.

Tetraodon nigroviridis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Peleosteii; Euteleostei; Acanthomorpha; Acanthopterygii; Peleosteii; Eutraodonicidea; Tetraodonidea; Tetraodonidea; Tetraodonidea; Tetraodonidea; Tetraodonidea; Genesostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodonidea; Tetraodonidea; Tetraodonidea; Tetraodonidea; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Genesosteii; Gene
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Direct Submission
Submitted (Un-NUG-2004) Genoscope - Centre National de Sequencage : 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
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| AATAAGAAGAATAAAGAGATTAAAATGATGGAAAAAAATTAAAAATTCAAAAGAAAAC
                                                                                                                                                                                                                                                                                  GlyPheLysGluAlaLeuSerAspAspValThrLysGlyLeuSerLysTyrLeuLysGly
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                                                                                               IlelleAlaAspAsnAsnArgHisLysGlyIleTyrLysAspLeuAsnLysIleAlaPro
                                                                                                                                                                                                                                               Thrile------GlubeutysSerPheAspGlyAspTyrAsnGluAsnIle
                                                                                                                                                                                                                                                                                                                                          AspAlaPheLysThrIleSerLysAlaLeuGlyLysGluGluGluGluGly-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                  LysLysArgLeuGluHisAspLysLysIleGluGluTyrLysLysLysGluIleThrMet
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TGG-----AGTTTAAAGACACTGAACATGAAAGAAAAGGAAAAGAAAAGAAAAGTGTT
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CR650378
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
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BW253010 BY253010 684 bp mRNA linear EST 09-NOV-2002 BW253010 Nori Satoh unpublished cDNA library, tailbud embryo Ciona intestinalis cDNA clone citb094pl5 5', mRNA sequence.
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bukaryota, Metazoa, Chordata, Urochordata, Ascidiacea, Enterogona,
Phlebobranchia, Cionidae, Ciona.
1 (bases 1 to 684)
Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
Expressed genes in Ciona intestinalis (2002c)
                                         484 ACAAAGTTCATTGAAGAAAACAGAGAGAAGTTTACTCAGTTGGACTTACAAGATGTTGAC 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----GAGGAAAAGGAGAAAA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         160 AlaPheLysThrIleSerLysAlaLeuGlyLysGluGluGluGlyLysLysArgLeuGlu 179
                                                                                                                                                                                                                                                      200 ValLeuProAlaValAlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrVal 219
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                                                                                                                                                                                                                                                                                                                                                                                                                          240 LeuSerLysTyrLeuLysGlyProTyrLeuGlnMetAsnThrGluThrLeuSerGlnVal 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    280 GluLeuGluLyBABpProValTrpLyBLyBLeuABnAlaValLyBABnGlnArgValAsp 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
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/dlome="citb094p1s"
/tissue_type="whole animal"
/dev_stage="tailbud embryo"
/clome_lib="Nori Satoh unpublished cDNA library, tailbud
                                                                                                                      424 ACTCGTGAGAAACTGAAAACACTCAAAAAGGCAAAGTTAAAAAACTGCAAAAACGCTTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      317 GluMetAlaLysGluLeuValGluLeuSerLysLysAspSerLysLysAspAsnLys 335
                                                                                                                                                                    180 GluHisAspLysLysIleGluGluTyrLysLysGluIleThrMetAspLysAsnGlnLys
                                                                                                                                                                                               260 AsnProGluArgMetPheIleMetThrAsnLysAlaSerSerAsnGluProSerLeuLys
142 AlaProThrileGlu-----LeuLysSerPheAspGlyAspTyrAsnGluAsnIleAsp
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Location/Qualifiers
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/organism="Ciona intestinalis"
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Tel: 81-75-753-4081
Fax: 81-75-705-1113
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Department of Zoology
Kyoto University
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                                                                                                                        AL854856 AGC-egg Xenopus tropicalis cDNA clone TEGG004£24 3', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hinxton. Cambridgeshire, CBIO 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenobus tropicalis EST project 2001
TROPICALIS SEQUENCE ID: TEGG004£24.qlkT7
Sequencing primer: T7
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
CDNA was oligo dT primed from Sug of poly A+ RNA from egg.
ECORI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end.
Vector: pCS107; Site 1: ECORI; Site_2: NotI
HOST: Escherichia coli XL1-blue.
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                                                                                                                                                                                                                                               Xenopus tropicalis (western clawed frog)

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Xenopodinae; Xenopus; Silurana.

1 (bases 1 to 673)

1 (bases 1 to 673)

Croning, M.D.R., Ashurst, J.L., Taylor,R., Zorn,A.M. and Rogers,J.

Sanger Xenopus tropicalis EST project 2001 (11_2003)

On Sep 15, 2002 this sequence version replaced gi:22875075.

Contact: Taylor R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pGS107; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dT primed from 5ug of poly A+ RNA from egg. EcoRI.NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="TEgg004f24"
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60
42
106
51
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Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Xenopus tropicalis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches:
Indels:
                        AAGGTGTGCAACCCCATCATCACAAGATG 1185
Lys-----AspProValTrpLysLysLeu 290
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                                                                                                                                                                  sequence.
AL854856
AL854856.2 GI:38630328
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115.50
39.38%
23.17%
6.83%
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Sanger Institute
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Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Cionidae; Ciona.

1 (bases 1 to 690)

2 satou Y. Shin-i,T. Kohara,Y. and Satoh,N.

Expressed genes in Ciona intestinalis (2002c)

Unpublished (2002)

Contact: Nori Satoh

Department of Zoology

Kyoto University

Sakyo-ku, Kyoto, Kyoto 606-8502, Japan

Fat: 81-75-753-4081
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127 CAATCCCAAATATTCACCACTTACTCGGACAACCAACCAGGGTGTGATCCAAGTGTAC 186
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                                                                                                                                                                                                                                                                                                                                /tissue_type="whole animal"
/dev stage="tailbud embryo"
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embryo"
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Conservative:
Mismatches:
Indels:
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Location/Qualifiers
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/db_xref="taxon:7719"
/clone="citb073p02"
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BW254793.1 GI:24834711
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BW235942 Nori Satch unpublished cDNA library, tailbud embryo Ciona intestinalis cDNA clone citb052c24 5', mRNA sequence.
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                                                      -------AlaProThrIleGluLeuLysSerPheAspGlyAspTyr 154
                                                                                                                           AsnGlu-----AsnIleAspAlaPheLysThrIleSerLysAlaLeuGlyLysGluGlu 172
                                                                                                                                                182
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357 AAGATCACAATCACCAACGACAAAGGTCGTCTTAGCAAGGAAGATATTGAGCGGATGGTG 416
                                                                                                                                                                                                                                                                      LyslyslleglugluTyrLysLysGlulleThrMetAspLysAsnGlnLysValLeuPro 202
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Phlebobranchia; Cionidae; Ciona.
1 (bases 1 to 700)
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/tissue type="whole animal"
/dev_stage="tailbud embryo"
/clone_lib="Nori Satch unpublished cDNA library, tailbud
embryo"
 GAGGTGAACGTACGATGACCAAGGACAACATACTTGGTAAGTTCGAGCTCTCCGGC
                                                                          417 AACGAAGCCGAGAAATATAAGGAAGAA-----GATGAGAAGCAGAAG-----GAG
                                                                                                                                                                                                                                                                                                                                                                                                                                           609 AACCAG------ACTGCCGAAAAGGACGAATATGAATTCCAACAAAAAGAACTT
                                                                                                                                                                                                 173 Glu-------GlyLysLysArgLeuGluGluHisAsp--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 262 GluArgMetPhelleMetThrAsnLysAlaSerSerAsnGluProSerLeuLysGluLeu
                                                                                                                                                                                                                                                                                                                                                                                                                    223 LeuSerGlnLeuGlyPheLysGluAlaLeuSerAspAspValThrLysGly---LeuSer
                                                                                                                                                                                                                                                                                                                                                                    Satou, Y., Shin-i, T., Kohara, Y. and Satoh, N. Expressed genes in Ciona intestinalis (2002c) Unpublished (2002)
Contact: Nori Satoh
Department of Zoology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: satch@ascidian.zool.kyoto-u.ac.jp
Location/Qualifiers
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Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
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/db_xref="taxon:7719"
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Ciona intestinalis
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BW222839 Nori Satoh unpublished cDNA library, larva Ciona intestinalis cDNA clone cilv051j23 5', mRNA sequence.
                                                                                                 547 GACGAAGATAAGTCAGCGATTCTTAACAAAGCTAAAGAAGTTTTGGACTGGTTGGAAAAT 606
                                                                                                                                                                 607 AACCAG------ACTGCGGAAAAGGACGAATATGAATTCCAACAAAAAGAACTT 654
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Publazyota, Metazoa, Chordata, Urochordata, Ascidiacea, Enterogona,

Phlebobranchia, Cionidae, Ciona.

1 (bases 1 to 692)

Satou, Y., Shin-i,T., Kohara,Y. and Satoh,N.

Expressed genes in Ciona intestinalis (2002c)
LeuSerGlnLeuGlyPheLysGluAlaLeuSerAspAspValThrLysGly---LeuSer 241
                                                                   242 LysTyrLeuLysGlyProTyrLeuGlnMetAsnThrGluThrLeuSerGlnValAsnPro 261
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129 CAATCCCAAATATTCACCACTTACTCGGACAACCAAGCTGTGTTGATCCAAGTGTAC 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
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/clone="cilv051j23"
/tiseue_type="whole animal"
/dev_stage="larva"
/clone_lib="Nori Satoh unpublished cDNA library, larva"
                    262 GluargMetPheIleMetThrAsnLysAlaSerSerAsnGluProSerLeuLysGluLeu
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Mismatches:
Indels:
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Location/Qualifiers
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655 GAGAAAATTGCCAACCCTATTATGACTAAACTT 687
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Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
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Department of Zoology
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BW222839
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109 LysGlnProAsnLeuGluGluIleSerLysLeuLysProAspLeulleileAlaAspAsn 128
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Eukaryota, Metazoa, Chordata, Urochordata, Ascidiacea, Enterogona, Phlebobranchia, Cionidae, Ciona.

1 (bases 1 to 702)
Satou,Y., Shin-1,T., Kohara,Y. and Satoh,N.
Expressed genes in Ciona intestinalis (2002c)
Unpublished (2002)
Contact: Nori Satoh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 GGAGGAGTGATGACAGCTTTG-----ATCAAGAGAAACACGACCGTCCCAACCAA 118
                                                                                                                                                                                                                /mol_type="mRNA"
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/db_xref="taxon:719"
/clone="citbo76c05"
/tissue_type="whole animal"
/dev_stage="tailbud embryo"
/clone_lib="Nori Satch unpublished cDNA library, tailbud embryo"
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Matches:
Conservative:
Mismatches:
                                                                                                                   Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-75-1113
Email: satch@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glu--------GlyLysLysArgLeuGluGluHisAsp-------182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 LysLysIleGluGluTyrLysLysGluIleThrMetAspLysAsnGlnLysValLeuPro
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                                                                                                                                                                  ValAspAlaLeuValAlaLeuAspValLysProValGlyIleAlaAspAspAsnLysLys
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                                                   Matches:
Conservative:
Mismatches:
Indels:
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Ciona intestinalis
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Best Local Similarity:
Query Match:
DB:
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BW055754 Nori Satoh unpublished cDNA library, blood cells Ciona intestinalis cDNA clone cibd084g20 5', mRNA sequence.
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                                                                                                          155 AsnGlu-----AsnIleAspAlaPheLysThrIleSerLysAlaLeuGlyLysGluGlu 172
                                                                                                                                                                                                                                                                                                                           203 AlaValAlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPhe 222
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Phlebobranchia, Cionidae, Ciona.
1 (bases 1 to 753)
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/mol_type="mRNA"
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                                                                                                                                 517 -------CTTAAATCAACGGTGGAGGATGACAAAGTGAAAGATAAAATTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 262 GluargMetPhelleMetThrAsnLysAlaSerSerAsnGluProSerLeuLysGluLeu
202 GAGGGTGAACGTACGATGACCAAGGACAACAACATACTTGGTAAGTTCGAGCTCTCCGGC
                                     -------AlaProThrIleGluLeuLysSerPheAspGlyAspTyr
                                                        173 Glu------GlyLysLysArgLeuGluGluHisAsp--------
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Expressed genes in Ciona intestinalis (2002)
Unpublished (2002)
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Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satch@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
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Department of Zoology
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Ciona intestinalis
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BW441129.1 GI:48494172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .713
/organism="Ciona intestinalis"
/organism="Ciona intestinalis"
/db_tref="taxon.7719"
/clone="cijv044124"
/tissue_type="whole animal"
/clone lib="whorisatoh unpublished cDNA library, juvenile whole animal"
                                                                                                                                                                                                                                                                                                                                                                                           Ciona intestinalis
Ciona intestinalis
Ciona intestinalis
Bukaryotes, Metazoa, Chordata; Urochordata; Ascidiacea, Enterogona;
Phlebobranchia; Cionidae; Ciona.
1 (bases 1 to 713)
Satou,Y., Nakayama,A., Shin-i,T., Kohara,Y. and Satoh,N.
Expressed genes in Ciona intestinalis (2004b)
                                                                          598
                                                                                                                                              646
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CAATCCCAAATATTCACCACTTACTCGGACAACCAACCAGGGTGTGTTGATCCAAGTGTAC 201
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 ------CTTAAATCAACAGTGGAGGATGACAAGTGAAAGATAAAATTTCA 538
                                     261
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                                                              262 GluargMetPheIleMetThrAsnLysAlaSerSerAsnGluProSerLeuLysGluLeu
                                                                                                                                  :::
599 AACCAG------ACTGCCGAAAAGGACGAATATGAATTCCAACAAAAGAACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ValAspAlaLeuValAlaLeuAspValLysProValGlyIleAlaAspAspAsnLysLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Nori Satch
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-763-4081
Fax: 81-75-765-1113
Email: satch@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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647 GAGAAAATTGCCAACCCTATTATGACAAAACTT 679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----GAGGAGCTGAGGAGTAAGCAGAGGTGTCTGGAGCGCGAGCAGCAGCAGAGGTG 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GluGluTyrLysLysGluIleThrMetAspLysAsnGlnLysValLeuProAlaValAla 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87 LysLysAsnArglleIleLysProLeuArgAspLysIleGlyLysTyrThrSerValGly 106
                                                                                                                                  Bonaldo, Ph.D. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) bnA Sequencing by: Incyte Genomics, Inc. Clone distribution: NCI-CGAP clone distribution information can l found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov c column: 07 High quality sequence start: 51 High quality sequence stop: 950. Location/Qualifiers
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106 AAGGCAGACGAGCTCAGCAAGCAGCTGAAGGACCTGTCCCAAAAGTACAGCGACGTGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ThrarglysGlnProAsnLeuGluGluIleSerLysLeuLysProAspLeuIleIleAla
                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                        NIH LOADER I LO JOIN NOT NIH GOV/.
NIH MAGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
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                                                                           Contact: Robert Strausberg, Ph.D.

    .981
    /organism="Mus musculus"

                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/strain="CZECH II"
                (bases 1 to 981)
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115.50
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                                                             Unpublished (1999)
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BI905625 IG:16168168
                                                                                                                                                                                                                                        GGAGGAGTGATGACAGCTTTG-----ATCAAGAGAAACACCACCGTCCCAACCAAA 188
                                                                                                                                                                                                                                                                                                    249 GAGGGTGAACGTACGATGACCAAGGACAACATACTTGGTAAGTTCGAGCTCTCCGGC 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                         Glu------GlyLysLysArgLeuGluGluHisAsp--------
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522 AAGATTCAAGCGAAGAACGGTCTCGAATCTTATGCGTTCAAC--------
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GAGAAAATTGCCAACCCTATTATGACAAAACTT 749
                                                                             Indels:
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Best Local Similarity:
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DB:
   Alignment Scores:
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TION Tetraodon nigroviridis full-length cDNA.

TORN 7813171.

CR731171.

CR731171.

GR731171.

GR73171.1

SHTC; CDNA; full-length; Tetraodon nigroviridis.

Tetraodon nigroviridis

ENKaryota; Metazas, Chordata; Craniata; Vertebrata; Euteleostemi;

Actinopterygii; Neopterygii; Percomorpha;

Acanthomorpha; Acanthopterygii; Percomorpha;

Tetradontoidea; Tetraodontidae; Tetraodon.

E (bases I to 1120)

Genoscone
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CTAAATAAAAATACAGAAAGAGATAAAAATCAGCAAAAAGAACATGTTAAAGAAGAAGAAATGC 570
                                                                                                                        236 ValThriysGlyLeuSeriysTyrLeuLysGlyProTyrLeuGlnMetAsnThrGluThr 255
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Direct Submission

Submitted (10-A004) Genoscope - Centre National de Sequencage

Submitted (10-A002004) Genoscope - Centre National de Sequencage

(E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

The sequences are based on single pass reads.

More information available at

http://www.genoscope.cns.fr/tetraodon.
                                                                                                                                              LeuSerGlnValAsnProGluArgMetPheIleMetThrAsnLysAlaSerSerAsnGlu
                                                                                                                                                                                                                                -----CAG
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                                                   216 AsnSerTyrValGlyGlnPheLeuSerGlnLeuGlyPheLysGluAlaLeuSerAspAsp
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/organism="Tetraodon nigroviridis"

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/db_xref="taxon:99883"
/tissue_type="fish"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuGluGluIle-----SerLysLeuLysProAspLeulleIleAlaAspAsnAsn 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTTGAGGAAATCCATTCTGTTAAGGAGCTCAAACCAGATGATGTTACTAAAACTGCTTTA 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       271 AGGAAAGAAATCAGTTTTGAAAAGTATGCAAAAGCCTAACAGCACTGCTGAGGAGCGA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            331 GCATTÁGCAAGACTGGCCACACCCTTTGCTTÁAGCAGAAAATCACAGCTATTAAAGÁG 390
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                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopus tropicalis
Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
Xenopodinae, Xenopus, Silurana.

1 (bases 1 to 785)

2 (croning, M.D. R., Ashurst, J. L., Taylor, R., Garrett, N. and Rogers, J. Canger Xenopus tropicalis EST project 2001 (2004)
                                                                                                                                                                  Contact: Croning MDR
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS SEQUENCE ID: TTbA033p07.plkSP6
This aequence is from a Xenopus Gene Collection (XGC) library
constructed by Nigel Garrett.
Seq primer: SP6.
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Matches:
Conservative:
Mismatches:
Indels:
                  Kenopus tropicalis (western clawed frog)
                                                                                                                                                                                                                                                                                                                                                                 /organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
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1353 AAGCGCAACACCACTTCCTACCAAGCAGACCCAGACCTTCACCACCTACTCTGACAAC 1412
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|GACGAGAAAACTCGCTGGGAAGATCAGTGACGATGACAAGCAGAAGATTTTGGACAAGTGC 1832
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1833 AACGAGGTCATCAGCTGGGTTGAAGAATCAG------ACTGCCGAGAAGGAC 1880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1641 AGTAAGGAGÁACATTGAGCGCATGCTGCAGGAAGCTGÁGAAGTÁCÁAGGCCGÁAGACGAC 1700
                                                                                                                                                                                                                                                                                                                                                                                                                                              1125 GGTTCCACTCGCATCCCAAAAATCCAGAAACTGCTCCAGGACTACTTCAACGGGAGGTTT 1184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             164 IleSeriysAlaLeuGlyLysGluGluGlu-------GlyLysLysArgLeu 178
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/tissue_type="Eyes"
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GATGCGGAGGCGGACGTGCTCTCTGAACCGGCGGATCCAGCTGGTGGAGGAGGAGCTG 401
                                              AsnLysIleAlaProThrIle------GluLeuLysSerPheAspGlyAsp 153
                                                                                                                                                                                                                                                                                                                                                                                                                     198 GlnLysValLeuProAlaValAlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSer 217
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Direct Submission

Submitted (10-A002-2004) Genoscope - Centre National de Sequencage : 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr) Frb sequences are based on single pass reads.

More information available at http://www.genoscope.cns.fr/http://www.genoscope.cns.fr/tetraodon.
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642 GAGGAACGCGCCGAGGCCGAGGCCAAATCTGGAGATCTT--------
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Contact: Genoscope
Genoscope - Centre National de Sequencage
Z rue Gastono Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: secref@genoscope.cns.fr, Web : www.genoscope.cns.fr
IMPORTANT: this sequence may contain errors. The Ciona intestinalis
library from which the clone was isolated may be contaminated with
CDNAs from bacteria or other Eukarya biscope.
Stazione A.Dohrn, Naples, Italy, and was prepared in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL666132 AL666132 ALFONA ALFONA LINEAR EST 11-JAN-2002 AL666132 directional larval cDNA library Ciona intestinalis CDNA Clone 002ZE10 5', mRNA sequence.
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                                                                                                                                                                                                                         203 AlaValAlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPhe
                                                                                                                                                                                                                                                  456 ---GTGTCTGCAAAGAATGGCCTGGAGTCCTATGCTTTCAAC--------
                                                                                                                                                                                                                                                                                                                                           -------ATGAAGTCAACTGTGGAGGATGAGAAGCTTGCTGGCAAGATCAGT
                                                                                                                                                                                                                                                                                                      223 LeuSerGlnLeuGlyPheLysGluAlaLeuSerAspAspValThrLysGly---LeuSer
                                                                                                     348 AAAATCACAATCACTAATGACAAAGGTCGTCTTAGTAAAGAGGACATTGAGCGCATGGTC
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                                                                173 Glu-------GlyLysLysArgLeuGluGluHisAsp
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Phlebobranchia, Cionidae, Ciona.
1 (bases 1 to 711)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryzinae; Oryzias.
E I (bases I to 707)
Kohara,Y., Shin-i,T., Kimura,T., Narita,T., Jindo,T. and Takeda,H.
Medaka EST Project in Takeda's lab
L Unpublished (2001)
Contect: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
Fax: 81-559-81-6855
                             1881 GAGTACGAGCATCAGCAGAAGGAGCTGGAGAAGGTGTGCAACCCCATCATCACAAAGATG 1940
                                                                                                                        BJ706325 BF01FFA CDNA Oryzias latipes CDNA clone MF01FFA017e14 5',
    273 SerAsnGluProSerLeuLysGluLeuGluLys-----AspProValTrpLysLysLysLeu 290
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Database :

Published Applications NA:*

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ALIGNMENTS

Sequence 2580, Application US/10724972A
Publication No. US20040147734A1
GENERAL INFORMATION:
APPLICANT: Doucette-Stamm, Lynn
APPLICANT: Bush, David
TITLE OF INVENTION: UUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PATH03-16
CURRENT APPLICATION NUMBER: US/10/724,972A
CURRENT FILING DATE: 2003-12-01
PRIOR FILING DATE: 1999-11-29 US-10-724-972A-2580

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GREEAL INVORVATION

APPLICANT: Wang, Liangsu
APPLICANT: Among, Carlos
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APPLICANT: Zamudio, Carlos
APPLICANT: Zykidd, Judith
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APPLICANT: Trawick, John
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PRIOR FILING DATE: 2000-03-23
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/230, 335
PRIOR APPLICATION NUMBER: 60/230, 335
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Staphylococcus epidermidis
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Matches:
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Mismatches:
Indels:
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                   PRIOR APPLICATION NUMBER: 09/134,001
PRIOR FILING DATE: 1998-08-13
PRIOR PELING NUMBER: 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-14
NUMBER 06 SEQ ID NOS: 7544
SEQ ID NO 2580
LENGTH: 1008
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Percent Similarity:
Best Local Similarity:
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20 GGAGTGGAACG-ATGAGAGGTCTAAAAACTTTTAGTATATTGGGATTAATAGTTGCCTTA 78
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Sequence 8156, Application US/09815242

Sequence 8156, Application US/09815242

Sequence 8156, Application US/09815242

Sequence 8156, Application US/09815242

APPLICAMT: Haselbeck, Robert

APPLICAMT: Chisen, Kari L.

APPLICAMT: Trawick, John D.

APPLICAMT: Trawick, John D.

APPLICAMT: Xu, H. Howard

ITILE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in FILE REPERBNCE: ELITRA, 01A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-12-22

PRIOR PILING DATE: 2000-12-22

PRIOR PILING DATE: 2000-12-22

PRIOR PILING DATE: 2000-12-22

PRIOR PILING DATE: 2000-12-6

PRIOR PILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SECTIVARE: PASESEE FOR WINDOWN Version 4.0

SEQ ID NO 8156

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Matches:
Conservative:
Mismatches:
Indels:
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; NAME/KEY: CDS
; LOCATION: (1)...(1014)
US-09-815-242-8156
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Best Local Similarity:
Query Match:
DB:
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APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Masolbeck, Robert
APPLICANT: Oblsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Zyskind, Judith
APPLICANT: Zyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Freseyth, R.
APPLICANT: Freseyth, R.
APPLICANT: Forsyth, R.
APPLICANT: Prosyth, R.
APPLICANT: ADMINER: 2001-20
FRICE REFERENCE: ELITRA.034A
CURRENT APLICATION NUMBER: 06/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-23
PRIOR FILING DATE: 2000-05-23
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                                  ProAspLeullellealaAspAsnAsnArgHisLysGlyIleTyrLysAspLeuAsnLys
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         GlubeuValGlubeuSerbysbysAspSerbys 331
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SeriysAlaLeuGlyLysGluGluGluGlyLysLysBrgLeuGluGluHisAspLysLys 184
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Mismatches:
Indels:
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Matches:
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-11-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
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PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-06
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PRIOR FILING DATE: 2001-02-06
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84.71%
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61 GAATCATCAACTAAAGATACTATTTCGGTAAAAGATGAAAATGGTACAGTACAT 120
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| TTAATAGTTGCCTTATTTTTAGTTGCAGCTTGTGGGTAATACGGATAATTCAAGTAAAAAA
                                                                                                                                                36 LysGluSerSerLysAspGlyValGluIleLysHisGluGluGlyThrThrLysValPro
                                                                                                 16 LeuleuPheValleulleAlaThrAlaAlaCysGlyAsnAsnSerSerSerser
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72.82%
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Best Local Similarity:
Query Match:
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US-09-815-242-4404

i Sequence 4404, Application US/09815242

i Sequence 4100-1520020061569A1

i GENERAL INFORMATION:

APPLICANT: Haelbeck, Robert

APPLICANT: Zyskind, Judith W.

APPLICANT: Zyskind, Judith W.

APPLICANT: Trawick, John D.

APPLICANT: Trawick, John D.

APPLICANT: Yamamoto, Robert T.

TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes

TITLE OF INVENTION: Prokaryotes

TITLE OF INVENTION: Prokaryotes

TITLE OF INVENTION WHERE: US/09/815,242

FILE REFERENCE: ELITAN, 011A

CURRENT APPLICATION WHERE: 60/191,078

FILE REFERENCE: ELITAN, 011A

CURRENT PELLING DATE: 2000-03-21

FRIOR FILING DATE: 2000-05-23

FRIOR PELLING DATE: 2000-10-23

FRIOR PELLING DATE: 2000-10-23

FRIOR PELLING DATE: 2000-11-27

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146 GluLeuLysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThrIleSer
                                                                                                                                              166 LysalareuglytysgluglugluglytystysakrgreuglugluHisasplystle
                                                                                                                                                                        186 GluGluTyrLygLygGluIleThrMetAspLysAsnGlnLysValLeuProAlaValAla
                                                                                                                                                                                                                                                                         535 GCGGAGATTAGAAAAAATTGAACAGAGTACGTTAAAAACTGCATTTGCATTCGGTATC
                                                                                                                                                                                                                                                                                                                206 AlalysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPheLeuSerGln
                                                                                          APPLICANT: ANAMATICAL PROPERTY AND THE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes FILE OF INVENTION: PROKARYOTES CURRENT FILING DATE: 2010-03-21 PRIOR PELICATION NUMBER: 60/206,848 PRIOR FILING DATE: 2000-05-23 PRIOR FILING DATE: 2000-05-26 PRIOR FILING DATE: 2000-05-26 PRIOR PRICHED DATE: 2000-05-26 PRIOR PRICHED DATE: 2000-10-23 PRIOR PRICHED DATE: 2000-10-23 PRIOR PRICHED DATE: 2000-10-23 PRIOR PRICHED DATE: 2000-10-23 PRIOR PRICHED DATE: 2000-10-23 PRIOR FILING DATE: 2000-11-27 PRIOR FILING DATE: 2000-11-27 PRIOR FILING DATE: 2000-11-27 PRIOR FILING DATE: 2000-11-27 PRIOR PRICHED DATE: 2000-11-27 PRIOR PRICHED DATE: 2000-11-27 PRIOR PRICHED DATE: 2000-11-27
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Yamamoto, Robert T.
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
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Trawick, John D.
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                                                                                                 APPLICANT: HEBELDECK, NOUTE,
APPLICANT: 298kind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Tyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Tramicot, Robert T.
APPLICANT: Vanamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-11-22
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Matches:
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Indels:
Gaps:
                   Sequence 4194, Application US/09815242
Patent No. US20020061S69A1
GENERAL INFORMATION:
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Alignment Scores:
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|GCGGAGATTAGAAAGAAAATTGAACAGAGTACGTTAAAAACTGCATTTGCATTCGGTATC 588
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                                                                                                                                                                                                                        ArgGlyLeuLysIleLeuSerValIleGlyLeuLeuPheValLeuIleAlaThrAlaAla
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Matches:
Conservative:
Mismatches:
Indels:
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SCPTWARE: FRACESC for Windows Version 4.0
; SEQ ID NO 8024.
; ERWITH: 960
; TEWCHI: 960
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(960)
US-09-815-242-8024
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                                                                                                                                                                                                                                                                                             Sequence 301, Application US/10470048B
Publication No. US20050037444A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ANTIGENS TO A SPECIFIC PATHOGEN
TITLE OF INVENTION: ANTIGENS TO A SPECIFIC PATHOGEN
FILE REFRENCE: SONN:03510S
CURRENT APPLICATION NUMBER: US/10/470,048B
CURRENT PILING DATE: 2003-07-25
NUMBER OF SEQ ID NOS: 603
SOFTWARE: PATENTIN version 3.1
SEQ ID NO 301
LENGTH: 957
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TTAGCCACTGACGGAAAAAACGGACAAAAATAGAACGAAATTC------ATTGAT
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; ORGANISM: Staphylococcus aureus
US-10-470-048B-301
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APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yau, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: 08/10/282,122A
CURRENT PILING DATE: 2008-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-11-27
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550 GAACAGAGTACGTTAAAAATCTGCATTTGCATTCGGTATCTCAAGAGCAGGTATGTTTATT 609
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                                                                                                                                                                                                        SerAspAspValThrLysGlyLeuSerLysTyrLeuLysGlyProTyrLeuGlnMetAsn 252
                                                                                                                                                                                                                                                             ThrGluThrLeuSerGlnValAsnProGluArgMetPhelleMetThrAsn----LysAla 271
                                                                              GluGlyLysLysArgLeuGluGluHisAspLysLysIleGluGluTyrLysLysGluIle 192
 429
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Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Waith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
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Ohlsen, Kari
Zyskind, Judith
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                                                                                  File
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Matches:
Conservative:
Mismatches:
Indels:
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PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2011-02-16
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILIOR DATE: 2011-02-16
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SOFTWARE: Patentin version 3.1
LENGTH: 960
                                                                                                                                                                  , ORGANISM: Staphylococcus aureus US-10-282-122A-7949
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5 ValArgGlyLeuLysIleLeuSerValIleGlyLeuLeuPheValLeuIleAlaThrAla 24
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Sequence 135107, Application US/10282122A

Sequence 135107, Application US/10282122A

Sequence 135107, Application US/10282122A

Sequence 135107, Application US/10282122A

APPLICANT: Wang, Liangu

APPLICANT: Malone, Cdery

APPLICANT: Malone, Cdery

APPLICANT: Malone, Cdery

APPLICANT: Malone, Cdery

APPLICANT: Malone, Cdery

APPLICANT: Malone, Cdery

APPLICANT: Transity, Judith

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APPLICANT: Transity, Judith

APPLICANT: Malone, Cdery, John

APPLICANT: Malone, Cdery, John

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APPLICANT: Malone, Cdery, John

APPLICANT: Transity, Judith

APPLICANT: Malone, Cdery, John

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APPLICANT: Malone, Cdery, John

APPLICANT: Malone, Cdery, John

APPLICANT: Malone, Cdery, John

PRIOR PELING DATE: 2000-03-21

PRIOR PELING DATE: 2000-05-35

PRIOR PELING DATE: 2000-05-35

PRIOR PELING DATE: 2000-01-23

PRIOR APPLICATION NUMBER: 60/22, 79

PRIOR APPLICATION NUMBER: 60/22, 79

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PRIOR AP
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253 ThrGluThrLeuSerGlnValAsnProGluArgMetPhelleMetThrAsn---LysAla 271
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US-10-282-122A-35107
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APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Allone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Malone, Kari
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
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APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANTON NUMBER: 60/191, 078
PRIOR PILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/230, 335
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
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25 AlaCysGlyAsnAsnSerSerSerBanSer------SerLysGluSerSerLys
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; Publication No. US20040029129A1
; GENERAL INFORMATION:
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487 CAGGATATTGCGGACATCGCCAAA-----ACGTTACCGAAAGGGAAAAAGGGATTATC
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PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION VUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-16
Remaining Prior Application data removed - S
NUMBER OF SEQ ID NOS: 78614
SEQ ID NO 30706
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US-10-282-122A-30706
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                    301 LeuAspArgAspLeuTrpAlaArgSerArgGlyLeuIleSerSerGluGluMetAlaLys
                                                                                   Sequence 2066, Application US/09974300
; Sequence 2066, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
    APPLICANT: Berka, Randy M.
    APPLICANT: Clausen, ID Groth
    TITLE OF INVENTION: Expression
    TITLE OF INVENTION: Expression
    TITLE OF INVENTION: Expression
    TITLE OF INVENTION: Expression
    TITLE OF INVENTION: Expression
    FILE REFERENCE: 10085.500-US
    CURRENT FILING DATE: 2001-10-05
    PRIOR PILING DATE: 2001-10-05
    PRIOR PILING DATE: 2000-10-06
    PRIOR PILING DATE: 2000-10-06
    PRIOR FILING DATE: 2000-10-07
    PRIOR FILING DATE: 2000-10-07
; RIOR APPLICATION NUMBER: 60/279,526
    PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
    SOFTWARE: FastESQ for Windows Version 4.0
; SEQ ID NO 2066
    LENGTH: 801
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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862 GAAGTCCAAGACTTTGTAACGAAATCCGCCAAA 894
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Query Match:
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Pred. No.:
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ed. No.: obse: srcent Simil. set Local Sil s	Qy 250 GlnMetAsnThrGluThrLeuSerGlnValAsnProGluArgMetPheilemetThrAsn 269 : : : :	## ## ## ## ## ## ## ## ## ## ## ## ##	Craig A. Rosen Steven C. Barash Michael R. Fannon TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences CORRESPONDENCES. 5256 CORRESPERT: 9410 Key West Avenue STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA ZIP: 20850	COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 466/33 OPERATING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII Text CURRENT APPLICATION DATA: PILING DATE: 27-Dec-2002 PRIOR APPLICATION NUMBER: 08/956,171 FILING DATE: October 20, 1997 APPLICATION NUMBER: 06/009,861 FILING DATE: January 5, 1996 APPLICATION NUMBER: 08/781,986 FILING DATE: January 3, 1997 ATTORNEY/AGENT INFORMATION:
Db 363 GAACATAAACAAAAGCTGGATGAATTGAAACAGAAATTCGGCAGCCGGAAACAGAGC 419 Qy 200 ValleuProAlaValAlaAlaLy8SerGlyLeuLeuAlaHi8ProSerAsnSerTyrval 219 i::	Qy 279 LysGluLeuGluLysAspProValTrpLysLysLeuAsnAlaValLysAsnGlnArgVal 298 1::::::::::::::::::::::::::::::::::::	RESULT 13 US-08-781-986A-355 Sequence 355, Application US/08781986A Publication No. US20030054436A1 GENERAL INFORMATION: APPLICANT: Charles Kunsch TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences NUMBER OF SEQUENCES: 5255 CORRESPONDENCE ADDRESS: ADDRESSEE: Human Genome Sciences, Inc. STRRET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA	TE THE TENE	REGISTRATION NUMBER: 90.446 REFERRNCE/DOCKET NUMBER: PB248PP REFERRNCE/DOCKET NUMBER: PB248PP TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504 TELEFAX: (301) 309-8512 INFORMATION FOR SEQ ID NO: 355: SEQUENCE CHARACTERISTICS: LENGTH: 668 base pairs TYPE: nucleic acid STRANDEDNESS: double TYPE: nucleic acid STRANDEDNESS: double TYPE: TOPOLOGY: linear US-08-781-986A-355 Alignment Scores:

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Percent Similarity:
Best Local Similarity:
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Publication No. US20040029129A1

Publication No. US20040029129A1

GENERAL INFORMATION:
APPLICANT: Mand, Liangsu
APPLICANT: Malone, Cherlo
APPLICANT: Malone, Cherl
APPLICANT: Malone, Cherl
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Yaskind, Judith
APPLICANT: Yaskind, Judith
APPLICANT: Yaskind, Judith
APPLICANT: Yasmoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
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APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Wi, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA, 034A

CURRENT APPLICATION NUMBER: US/10/282,122A
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Matches:
Conservative:
Mismatches:
Indels:
RECISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248PLD1
TELEPHONE: (240) 314-1224
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 355:
SEQUENCE CHARACTERISTICS:
LENGTH: 668 base pairs
TYPE: nucleic acid
STRANDENNESS: double
                                                                                                                                     TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 355:
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Query Match:
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US-10-282-122A-19870
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165 SerLysAlaLeuGlyLysGluGluGluGlyLysLysArgLeuGluGluHisAspLysLys 184
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PLILING DATE: 2000-03-21
PRIOR PLILING DATE: 2000-05-26
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PRIOR FILING DATE: 2000-05-26
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; ORGANISM: Enterobacter cloacae
US-10-282-122A-19870
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Percent Similarity: 57.45% Best Local Similarity: 35.46%	Query Match: 27.22% DB:
 TATTCAACCTGCATGAGGGACCGGCAGCGTGCTGGCT 603	ysGluAlaLeuSerAspAspValThrLysGlyLeuSerLysTyrLeu 244

ddur.2000-82/6-42/-01-8n

603	244	263	693	744	303	323	864		
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PATTC	raGlu.		rAsn	CTGCTGGTTGCCCACTATCGC	BLYBI : GATAT	gser	GATGC		16. 15-242-6372. Ince 6372, Application US/09815; to No. US20020061569A1 AL INFORMATION: ICANT: Haselbeck, Robert ICANT: Haselbeck, Robert ICANT: Asilon, Daniel ICANT: Trawick, John D. ICANTE: Tra
CAGC	PheLy CTG	TyrLe	MetTh	GCCCA	TrpLy ::	Alaar 	30000		6 5-242-6372 No. US2002006156941 L INFORMATION: CANT: Haselbeck, Robert CANT: Ohlsen, Kari L. CANT: Ohlsen, Kari L. CANT: Ohlsen, Kari L. CANT: Trawick, John D. CANT: Trawick, John D. CANT: Trawick, John D. CANT: Trawick, John D. CANT: Trawick, John D. CANT: Trawick, John D. CANT: Trawick, 2001 D. CANT: Xu, H. Howhert GANT: Xu, H. H. Howhert GANT: Xu, H. Howhert GANT: Xu, H. H. Howhert GANT: Xu, H. Howhert GANT: Xu, H. Howhert GANT: Xu, H. Howhert GANT: Xu, Haselber GANT: Xu, H. Howhert GANT: Xu, H. Howhert GANT: Xu, Hare GANT: Xu, H. Howhert GANT: Xu, H. Howhert GANT: Xu, H. Howhert GANT: Xu, H. Howhert GANT: Xu, H. Howhert GANT: Xu, H. Howhert GANT: Xu, H. Howhert GANT: Xu, H. Howhert GANT: Xu, H. Howhert GANT: Xu, H. Howhert GANT: Xu, H. Howhert GANT: Xu, H. Howhert GANT: Xu, H. Howhert GANT: Xu, H. Howhert GANT: Xu, H. Howhert GANT: Xu, H. Howhert GANT: Xu, H. Howhert GANT: Xu, H. Howhert GANT: Xu, H. Howhert GANT:
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TCAO	GlnL TCTC	LysG.	MetP	CTGC	AspP1	Asple	AACGCCT GluLeu	AAAATC	6. 5-242-6372. 10. USZO02006 LINFORMATION: (CANT: Haselbec. (CANT: Zyskind. (CANT: Zyskind. (CANT: Zyskind. (CANT: Zyskind. (CANT: Zyskind. (CANT: Zyskind. (CANT: Yamamoc. (CANT: Yamamoc. (CANT: Yu, H. OF INVENTION: OF INVENTION: NT APPLICATION NT FILING DATE: APPLICATION NG STO. THEN: T
544	225	245	264	694	284		324	865	-242-6 -6 372 -6 372 -6 373 -6 374 -7
									ESULT 16 S-09-815-242-6372 Sequence 6372, Application US/09815 Patent No. US20020061569A1 APPLICANT: Haealbeck, Robert APPLICANT: Ohlsen, Kari L. APPLICANT: Trawick, John D. APPLICANT: Trawick, John D. APPLICANT: Yamamotck, John D. APPLICANT: Trawick, John D. APPLICANT: Trawick, John D. APPLICANT: Trawick, John D. APPLICANT: Trawick, John D. APPLICANT: Trawick, John D. APPLICANT: Tamamotck, Robert T. APPLICANT: Trawick, John D. APPLICANT: Tamamotck, Robert T. APPLICANT: Tamamotck, Robert T. APPLICANT: Tamamotck, Robert T. APPLICANT: Tamamotck, Robert T. APPLICANT: Tamamotck, Robert T. APPLICANT: Tamamotck, 2000-05-05 CURRENT FILING DATE: 2001-03-21 PRIOR APPLICATION NUMBER: 60/207, PRIOR APPLICATION NUMBER: 60/225, 69 PRIOR FILING DATE: 2000-10-23 PRIOR PLING DATE: 2000-10-23 PRIOR PLING DATE: 2000-11-27 PRIOR APPLICATION NUMBER: 60/257, 99 PRIOR PLING DATE: 2000-12-22 PRIOR APPLICATION NUMBER: 60/257, 99 PRIOR FILING DATE: 2000-12-22 PRIOR PLING DATE: 2000-12-22 PRIOR PLING DATE: 2001-02-16 SEQ ID NOS: 14110 SEG ID NO 6372 LENGTH: 909 CRANISM: Escherichia coli FEATURE: NUMBER OF SEQ ID NOS: 14110 SEG ID NO 6372 LENGTH: 909 CRANISM: Escherichia coli FEATURE: NUMBER OF SEQ ID NOS: 14110 OGANISM: COS NUMBER OF SEQ ID NOS: 14110 OGANISM: COS NUMBER:
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Length: Matches:

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Alignment Scores: Pred. No.: Score:

	Percent Sim Best Local & Query Match DB:	Similarity: sal Similarity: stch:	57.45% 35.46% 27.22%	Conservative: Mismatches: Indels: Gaps:	62 104 16 4	
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	٠ خ ظ	65	PheValAspAlaLeu	ValAlaLeuAspvali	GluTyrSerPheValAspAlaLeuValAlaLeuAspValLysProValGlyIleAlaAsp	84
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_	Qy 14	S	LysSerPheAspGly	rPheAspGlyAspTyrAsnGluAsnI	leAspAlaPheLysThrIle	16
-	Db 37	376 CIGCIGCIL	 AAGTCCCGCAACGAA	 	:::	43
Ĭ	Oy 16	Ŋ	LeuGļyLysGluGlu	GluGluGļuGlyLysLysArgi	euGluGluHisAspLysLys	184
I	Db 43	9	:::[[GTGGGTAAAAAGCGA	 GAGATGCAGGCACGTC		495
Ū	0,	85 IleGluGlu	I	o.	lnLysValLeuProAlaVal	204
ч	Db 45	96 ATGGCGCAG	ATGCCGCAGTGGGCCAGCCAG	CTTCCCAAAGGGA	::: CTTCCCAAAGGACACGCGTGGCCTTTGGCACA	549
J	Qy 20	5 Ala	SerGlyLeuLeuAla	aHisProSerAsnSerTyrVal	yrValGlyGlnPheLeuSer	224
ц	Db 55	50 TCACGCGAA	CAGCAATTCAACCTG		 	609
J	Qy 22	5 GlnLeuGl	yPheLysGluAlaLeu	aLeuSerAspAspValThrL	ThrLysGlyLeuSerLysTyrLeu	244
Ц	Db 61	.o rcrcrcccrc	TG		AACGTTCCCGCTGCGATG	639
J	Oy 24	5 L	yProTyrLeuGlnMet/	GlnMetAsnThrGluThrLeuS :::	euSerGlnValAsnProGluArg	263
L	Db 64	0	CCATGCCGTCCATC	seccredácaacide	CGGGTGCGTCCATCCGTCCATCGGCTGGAGCAACTGCTGGCGGTCAATCCTGCCTG	669
OI I		4 MetPhe	<pre>MetPheIleMetThrAsnLysAlaS ::: :::</pre>	erSer	erAsnGluProSerLeuLysGluLeuGluLys	283
-	02 40	0	1	GAAGAGAGCA	GAAGAGAGCATTGTTÄÄÄCGCTGGCAACAA	750
OI E	Oy 28	4 -	rpLysLysLeuAsn	AlaValLysAsnGlnA	AspProValTrpLysLysLeuAsnAlaValLysAsnGlnArgValAspIleLeuAspArg	0
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י מ	81	a AACACCTGG				323
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Ω	Db 87.	1 AAAATC 876				
25	RESULT 17 US-10-282-12; Sequence 2; Publicatio; GENERAL IN;	ISSULT 17 IS-10-282-122A-20621 Sequence 20621, Applicati Publication No. US2004002 GENERAL INFORMATION: APPLICANT: Wang, Liangsu	lon US/10282 !9129A1	122A		

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700 crgcrggrrgcccacrarcgc-----gaadagagcarrgrraaacgcrggcaacaa 750
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                                                                                                                                                                                                    225 GlnieuglyPheLysGluAlaLeuSerAspAspValThrLysGlyLeuSerLysTyrLeu 244
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                                                                                    165 SerlysAlaLeuGlyLysGluGluGluGlyLysLysArgLeuGluGluHisAspLysLys 184
                                                                                                                           436 GGCGAAATGGTGGGTAAAAAGCGAGAGAGATGCAGGCACGTCTGGAACAACATAAAGAGAGG 495
                                                                                                                                                                     185 IleGluGluTyrLysLysGluIleThrMetAspLysAsnGlnLysValLeuProAlaVal 204
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  145 IleGluLeuLysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThrile
                                 205 AlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPheLeuSer
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TITLE OF INVENTION: NIMR COMPOSITIONS AND THEIR METHODS OF USE
FILE REPRENCE: PKZ-043
CURRENT APPLICATION NUMBER: US/10/893,671
CURRENT FILING DATE: 2004-07-15
PRIOR PRILING DATE: 2004-07-15
PRIOR PLILING DATE: 2001-03-08
PRIOR FILING DATE: 2000-03-10
PRIOR FILING DATE: 2000-03-10
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
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Matches:
Conservative:
Mismatches:
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Query Match:
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TILLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2000-02-20
PRIOR PLILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR PLILING DATE: 2000-03-21
PRIOR PLILING DATE: 2000-03-24
PRIOR PLILING DATE: 2000-03-26
PRIOR PLLING DATE: 2000-03-26
PRIOR PAPLICATION NUMBER: 60/207,727
PRIOR PLLING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PLILING DATE: 2000-10-23
PRIOR PLLING DATE: 2000-11-27
PRIOR PLLING DATE: 2000-12-22
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Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
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Forsyth, R.
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ORGANISM: Escherichia coli
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APPLICANT: Xu, H.
TITLE OF INVENTION: A.
TITLE OF INVENTION: A.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
CURRENT PELITRA DATE: 2003-02-20
CURRENT PELITRO DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PELING DATE: 2000-03-21
PRIOR PELING DATE: 2000-03-23
PRIOR PELING DATE: 2000-05-26
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US-10-282-122A-33236
Sequence 33236, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
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APPLICANT: Wang, Liangsu
APPLICANT: Malone, Carlos
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
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RESULT 21
US-10-278-946-15
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GENERAL INFORMATION:
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TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
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328 TATAACGACCTGGCCTGGCTCCGACGCTGATGTTGCCGTCACGCGGGGGAGGACTAT 387
                              AsnGluAsnIleAspAlaPheLysThrileSerLysAlaLeuGlyLySGluGluGluGluGly 174
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67 GGGAATTCAAATAAACAATCTGATAACAAAGATAAGGAAACAACTTCAATTAAACAT 126
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13 ATTAAAATGCTT----GTTGTTACGCTTGCTTCCTACTTGTT----TTAGCAGGATGTAGT
                                                                                                                                48 GluGluGlyThrThrLysValProLysHisProLysArgValValValLeuGluTyrSer
                                        28 AsnAsnSerSerSerAsnSerSerLysGluSerSerLysAspGlyValGluIleLysHis
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221 GlnPheLeuSerGlnLeuGlyPheLysGluAlaLeuSerAspAspValThrLysGlyLeu 240
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                                                               GCTTCAGTTGTTAACTTCCGTGCTGATCATACAAGAATTTATGCTGGTGGATATGCTGGT
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             -GATGCAAAAGCAAAGTATAAAGATGCATGGCCATTGAAA
                                                  ---SerTyrvalGly
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US-10-967-189-15
Sequence 15, Application US/10967189
Sequence 15, Application US/10967189
Sequence 15, Application No. US20050053995A1
GENERAL INFORMATION:
TITLE OF INVENTION: Staphylococcus aureus Genes and Polypeptides
TITLE OF INVENTION Staphylococcus aureus Genes and Polypeptides
CURRENT FILID DATE: 2004-10-19
FRICH APPLICATION NUMBER: US/10/967,189
CURRENT FILING DATE: 2002-10-24
FRICH APPLICATION NUMBER: US 09/930,217
FRICH APPLICATION NUMBER: US 09/930,217
FRICH APPLICATION NUMBER: US 60/086,682
FRICH APPLICATION NUMBER: US 60/080,296
FRICH FILING DATE: 1998-03-10
FRICH FILING DATE: 1998-03-20
FRICH FILING DATE: 1998-04-01
FRICH FILING DATE: 1998-04-01
FRICH FILING DATE: 1998-04-01
FRICH FILING DATE: 1998-05-07
NUMBER: OF SEO ID NOS: 22
SOFTWARE: PatentIn version 3.1
SEQ ID NO 15
LENGTH: 999
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Matches:
Conservative:
Mismatches:
Indels:
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253 CAAAAACCGAAATTCGAATACATAAAAATGATTTAAAAGATACTAAGATTGTAGGTCAA 312
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                  GENERAL INFUGENT: Simpson et al.

TITLE OF INVENTION: Staphylococcus aureus Genes and Polypeptides

FILE REFERENCE: PB46/1051

CURRENT APPLICATION NUMBER: US/10/278,946

CURRENT FILING DATE: 2001-024

PRIOR PILING DATE: 2001-04-24

PRIOR FILING DATE: 2001-04-24

PRIOR FILING DATE: 1999-03-18

PRIOR FILING DATE: 1999-03-10

PRIOR FILING DATE: 1999-03-10

PRIOR FILING DATE: 1999-04-01

PRIOR FILING DATE: 1998-04-01

PRIOR FILING DATE: 1998-04-01

PRIOR FILING DATE: 1998-04-01

PRIOR FILING DATE: 1998-05-07

SPRIOR FILING DATE: 1998-05-07

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PATENTIN VERSION 3.1

LENGTH: 999
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Matches:
Conservative:
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; ORGANISM: Staphylococcus aureus
US-10-278-946-15
US20030153733A1
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                                                                                73 GGGAATTCAAATAAACAATCATCTGATAACAAAGATAAGGAAACAACTTCAATTAAACAT 132
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                                                      28 AsnAsnSerSerSerAsnSerSerLysGluSerSerLysAspGlyValGluIleLysHis 47
                    19 ATTAAAATGCTT---GTTGTTACGCTTGCTTTCCTACTTGTT---TTAGCAGATGTAGT 72
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RESULT 23
US-08-781-986A-238

US-08-781-986A-238

; Sequence 238, Application US/08781986A
; Sequence 238
; Dublication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                          ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
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Conservative:
Mismatches:
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                                                                                                                                                             ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Benson, Bob
REGISTRATION NUMBER: 90,446
REPERENCE/DOCKET NUMBER: PB248PP
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8512
INFORMATION FOR SEO ID NO: 238:
SEQUENCE CHARACTERISTICS:
LENGTH: 3775 base pairs
                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
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ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
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DB:
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Percent Similarity:
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Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polymucleotides and Sequences NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        973 TATAAATCTTCATTAAAACTTATTGACGATTTATATGAA-----AAGTTAAAATTTGAA 1026
                     414
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583 TTCCAAAAA-----GATGCAAAGCAAAGTATAAAGATGCCATTGAAA 630
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GCTTCAGTTGTTAACTTCCGTGCTGATCATACAAGAATTTATGCTGGTGGATAHGCTGGT 690
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                                                                                                                                                                                                                                                                                                     241 SerLysTyrLeuLysGly-----ProTyrLeuGlnMetAsnThr---GluThrLeuSer 257
                                                                                                                                                                                                                                                                                                                                                     GlnValAsnProGluArgMetPheIleMetThrAsnLysAlaSerSerAsnGluProSer 277
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AsnAsnArgHisLysGlyIleTyrLysAspLeuAsnLysIleAlaProThrIleGluLeu
                                                                                    LysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThrIleSerLysAla
                                                                                                          ---TCTACTGATACAGTTTTCAAATTCAAA---GATACAACTAAGTTAATGGGGAAAGCT
                                                    TyrLysLysGlulleThrMetAspLysAsnGlnLysValLeuProAlaValAlaAlaLys
                                                                                                                                                                                                                                      SerGlyLeuLeuAlaHisProSerAsn---------SerTyrValGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
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STREET: 9410 Key West Avenue
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US-10-329-624-238
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61 ATTAAAATGCTT---GTTGTTACGCTTGCTTTCCTACTTGTT---TTAGCAGGATGTAGT 114
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Conservative:
Mismatches:
Indels:
                                                                                                                            APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAWE: MARK J. HYMAN
REGISTRATION NUMBER: 46,789
REGISTRATION NUMBER: PB248P1D1
TELECOMMUNICATION:
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                          APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NO: 238
                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 3775 base pairs
                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 238:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: double
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                                                                                                                                                                                                                      GlnValAsnProGluArgMetPheIleMetThrAsnLysAlaSerSerAsnGluProSer 277
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 582
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523 TTAGGGAAAGAAAAAGAAGCTGAAGATTTACTTAAAAAGTACGATGATAAAAGTAGCTGCA
                                                      TTCCAAAAA------GATGCAAAAGCAAAGTATAAAAGATGCATGGCCATTGAAA
                                                                                     ----SerTyrValGly
                                                                                                            188 TyrLysLysGluIleThrMetAspLysAsnGlnLysValLeuProAlaValAlaAlaLys
                                                                                        SerGlyLeuLeuAlaHisProSerAsn----
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PRIOR FILING DATE: 2000-03-21
PRIOR PELING DATE: 2000-03-21
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/200, 335
PRIOR PELING DATE: 2000-09-06
PRIOR PELING DATE: 2000-09-09
PRIOR PELING DATE: 2000-09-09
PRIOR PELING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242, 578
PRIOR PILING DATE: 2000-10-23
PRIOR PELING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9415, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Framinch, Rant
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Xu, H.
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194 MethsplysAsnGlnLysValLeuProAlaValAlaAlaLysSer------Gly 209
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643 ATCTTAACT-----GACAATTCTTTAGCTTTACAAGTTACAAAAATTAGGT-----
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PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 9415
LENGTH: 972
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1116
122
122
13
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Matches:
Conservative:
Mismatches:
Indels:
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391.00
51.93%
34.42%
23.14%
                                                                                                                                                                                                                TYPE: DNA ORGANISM: Bacillus anthracis
                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Qy 104 Ser		0y 144 Thr	Db 409 ACG	Db 469 Qy 180 GluF		Db 637 GGCT QY 240 LeuS	Db 682 ATCG	736	Qy 279 LysG Db 796 AAAG	Qy 299 AspI	Db 856 ACAT	Qy 318 MetA 		CURRENT APPLICA: CURRENT FILING I PRIOR APPLICATIO PRIOR FILING DAT	; PRIOR APPLICATIO ; PRIOR FILING DA! ; PRIOR APPLICATIO ; PRIOR FILING DA!	; NUMBER OF SEQ II ; SOFTWARE: CLBTON ; SEQ ID NO 7183 ; LENGTH: 2209	
	739	<pre>Qy 269 ABnLy8AlaSerSerAsnGluProSerLeuLy8GluLeuGluLy8AspProValTrpLy8 288 ::::::::::::::::::::::::::::::::::</pre>	Oy 289 LysLeuAsnalaValLysAsnGlnArgValAspIleLeuAspArgAspLeuTrpAlaArg 308 		GENERAL INFORMATION: APPLICANT: Berka, Randy M. APPLICANT: Clausen, ID Groth TITE OF INVENTION:	TITLE OF INVENTION: Expression	CURRENT FILING DATE: 2001-10-05 PRIOR APPLICATION NUMBER: 09/680,598 PRIOR FILING DATE: 2000-10-06	; FRICK AFFILING DATE: 2001-03-27; NUMBER OF SEQ. ; NUMBER OF SEQ ID NOS: 8481	; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 2061 ; LENGTH: 944 ; TYPE: DNA	; ORGANISM: Bacillus licheniformis US-09-974-300-2061		Fred. No.: 3.98-23 Length: 944 Score: 380.50 Matches: 109 Percent Similarity: 52.924 Conservative: 63 Best Local Similarity: 33.54% Mismatches: 128 Query Match: 22.51% Indels: 25 DB: 9 Gaps: 13 US-10-724-972A-6352 (1-335) x US-09-974-300-2061 (1-944)	Qy 8 LeuLysIleLeuSerValIleGlyLeuLeuPheValLeulleAlaThrAlaAlaCys 26	Oy 27 GlyAgnAgnSerSerSerBenSerSerLygGluSerSerLygAggGlyValGlu1le 45	Oy 46 LysHisGluGluGlyThrThrLysValProLysHisProLysArgValValValLeuGlu 65	Qy 66 TyrSerPheValAspAlaLeuValAlaLeuAspValLysProValGly1leAla 83 Db 181 TTTGGAATGCTTGACGCTTGATGAGCTTGGCTTAAGCGACCGCGTTGTCGGCCTTCCG 240	Oy 84 AspAspAsnLysLysAsnArgIleIleLysProLeuArgAspLysIleGlyLysTyrThr 103

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elleAlaAspAsnAsnArgHisLysGlylleTyrLysAspLeuAsnLyslleAlaPro 143
                                                                                                                     aPheLysThrIleSerLysAlaLeuGlyLysGluGluGlyLysLysLysArgLeuGlu 179
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GATCGACATTGAGCTTGACCAGAAGAACTACATGAACAGTTTTAAAGAAAAATACGAA 468
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|CGTCGGCGGACTAAAAGAGCCAGATTTTGAAAAATTGCTGAGCTTGAGCCTGATTTG
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VENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

VES: 790CIP3/US

LICATION NUMBER: US/10/450,763

ING DATE: 2001-03-06-11

AATION NUMBER: PCT/US01/08631

3 DATE: 2001-03-30

3 DATE: 2000-03-31

3 DATE: 2000-03-31

5 DATE: 2000-08-23

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Application US/10450763
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tTION:
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            2209
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            Length:
Matches:
Conservative:
Mismatches:
Indels:
                3.276-22
375.00
50.178
32.548
                                                       Percent Similarity:
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Query Match:
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Alignment Scores:
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3-10-450-763-8842 Sequence 8842, Application US/10450763

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NAME/KEY: SIMILAR
LOCATION: (1)..(654)
OTHER INFORMATION: 98% homologous to Escherichia coli K12 citrate-dependent iron
OTHER INFORMATION: transport, periplasmic protein, accession number AE000499, Smith-
OTHER INFORMATION: Waterman Score=1060.
PEATURE:
NAME:
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145 IleGluieulysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLy8Thrile 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165 SerLysAlaLeuGlyLysGluGluGluGlyDybLysArgLeuGluGluHisAspLysLys 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Publication No. US20050196754A1
GENERAL INFORMATION:
APPLICANT: Hyseq. Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR PLING DATE: 2000-03-31
PRIOR PLING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SEQ ID NO 8842
LIENGTH: 4392
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OTHER INFORMATION: n = a,t,c
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ORGANISM: Homo sapiens
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Query Match:
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Db 1732 GAACTCTCGTTCGCCGATGCGCTGGCCGTGGACGTCATCCCGATCGGTATTGCCGAC 1791	OY 85 ASDASHLYSEVSASHARGILSILELYSPROLEWARGASDLYSILEGIYLYSTYRTHRSER 104	ValGlyThrArgLy8GlnProAsnLeuGluGluIleSerLysLeuLysProAspLeuIle	1852 GICGGAACGCGCGCGCGCGCTGGAAGCCATTGCCGCTCTGAAACCAGACCTGATC 125 IleAlaAspAsnAsnAsGHisLysGlylleTyrLysAspLeuAsnLysIleAlaProThr	145	1972 CTGCTGCTTAAGTCCCGCAACGAAACCTACGCTGAAATTTGCAATCTGCGGCTATCATC	Db 2032 GGCGAAATGGTGGTAAAAAGCGAGAGATGCCAGGTCTGGAACAAAAAAAGGTGAAGAGAGAG	Qy 185 IleGluGluTyrLysElysGluIle 192 ::::::::::::::::::::::::::::::::::::	RESULT 30 US-08-781-986A-604	ີ່ດ່⊉	TITLE OF INVESTIGES AND SCA : TITLE OF INVESTIGES AND SEQUENCES : NUMBER OF SEQUENCES: 5255 : 5255 : CORPREDANDENCE AND SECUENCES	** ADDRESSER: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue	; CITY: Rockville ; STATE: Maryland ; COUNTRY: USA	; ZIP: 20850 ; COMPUTER READABLE FORM: ; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage	86/33 OS version 6.2	CORRENT APPLICATION DATA: 7 APPLICATION NUMBER: US/08/781,986A 7 FILING DATE:	CLASSIFICATION: 435 ; PRIOR APPLICATION DATA: ; APPLICATION NUMBER:	; FILING DATE: ; ATTORNEY/AGENT INFORMATION: ; NAME: Benson, Bob	; REGISTRATION NUMBER: 30,446 ; REFERENCE/DOCKET NUMBER: PB248PP ; TELECOMUNICATION INFORMATION: ; TELEPHONE: (3A1) 306-2604	(301) 309-851 R SEQ ID NO: RACTERISTICS:	; TYPE: nucleic acid ; STRANDEDNESS: double ; TOPOLOCY: Discase:	504	1.03e-18 334.00 milarity: 63.84%	37 85% Migmatches.
		604 TCTCTGGGGCTG		694 TCTATCCATGCAATTACGGTTACAACCACACCCTGTCTC	Oy 285 ProvalTrpLysLysLeuAsnAlayalLysAsnGlnArgValAspIleLeu 301	- 13 - 13 - 13	317	SULT 29	US-10-450-763-13139 ; Sequence 13139, Application US/10450763 ; Publication No. US20050196754A1	; GENERAL INFORMATION; ; APPLICANT: Hyseq, Inc ; TILLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES	; File KEFKERNER: 790CIP3/US CURRENT APPLICATION NUMBER: US/10/450,763 ; CURRENT FILING DATE: 2003-06-11	; PRIOR APPLICATION NUMBER: PCT/US01/08631 ; PRIOR FILING DAPE: 2001-30; ; PRIOR APPLICATION NUMBER: 00/1000000	; PRIOR FILING DATE: 2000-03-31 ; PRIOR APPLICATION NUMBER: 09/649,167 ; PRIOR FILING DATE: 2000-08-23	; NUMBER OF SEQ ID NOS: 60736 ; SEV ID NO 13139	; LENGTH: 2799 ; TYPE: DNA ; ORGANISM: Homo saniens	FEATURE: NAME/KEY: SIMILAR LOCATION: (181) (901)	CTHER INFORMATION: 73% homologous to Mus musculus Pro-Pol-dUTPase; OTHER INFORMATION: polyprotein, accession number Y12713, Smith-Waterman Score=892. US-10-450-763-13139	Alignment Scores: Pred. No.: 6.14e-20 Length: 2799	Percent Similarity: 68.92% Conservative: 33 Best Local Similarity: 46.62% Mismatches: 46 Query Match: 20.71% Indels: 0 DB:	ougs:) x US-10-450-763-13139 (1-2	Qy 45 IleLysHisGluGluGlyThrThrLysValProLysHisProLysArgValValValLeu 64		

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FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY, AGENT INFORMATION:
NAME: MARK J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMUNICATION IRFORMATION:
TELEPHONE: (240) 314-1224
TELEFRY: (301) 309-8439
INFORMATION FOR SEQ ID NO: 604:
SEQUENCE CHARACTERISTICS:
LENGTH: 2115 base pairs
                                                                                                                                                                                                                                                                             NO: 604:
                                                                                                                                                                                                                                                                               SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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334.00
63.84%
37.85%
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Best Local Similarity:
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US-08-781-986A-2556
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Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  470
                                                                                                                                                                                                                                                                                                                                                                                                                                           GluThrieuSerGlnValAsnProGluArgMetPhelleMetThrAsn---iysAlaSer 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             363 AAAAATAGAACGAAATTC-----ATTGATCCTGCAGTTTGGAAATCATTAAAA 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                292 AlavaliysAsnGlnArgValAspIleLeuAspArgAspLeuTrpAlaArgSerArgGly 311
                                                                                                                                                                                                                                                                                                                             183 AATGAAGATACATTTATGGGACAATTCTTAATTAAAATGGGTATTCAACCTGAAGTCAMA 242
                                                                                                                                                                                                                                                                                                                                                                         234 AspAspValThrLysGlyLeuSerLysTyrLeuLysGlyProTyrLeuGlnMetAsnThr 253
                                                                                                                                                                                                                                                                                                                                                                                           273 SerhanGluProSerLeuLysGluLeuGluLysAspPro---ValTrpLysLysLeuAsn 291
                                                                                                                                                                                                                                                          214 ProSerAsnSerTyrValGlyGlnPheLeuSerGlnLeuGlyPheLysGluAlaLeuSer 233
                                                                                                                                                                 174 GlyLysLysArgLeuGluGluHisAspLysLysIleGluGluTyrLysLysGluIleThr 193
                                                                                                                                                                                      194 MethspLyshsnGlnLysValLeuProAlaValAlaAlaLysSerGlyLeuLeuAlaHis 213
                                                                                              TyrkenGlukenilekepalaphetysThrileSertysAlaLeuGlytysGluGluGlu 173
                                                                                                                 411 derigidadadanaacadagirrargacgirgaecgadataagiggirgadateaagggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeulleSerSerGluGluMetAlaLysGluLeuValGluLeuSerLysLys 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectter 486/33
COMPUTER: HP Vectter 486/33
COMPUTER: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US110/329,624
FILING DATE: 27-Dec-2002
FRIOR APPLICATION DATA:
                                                               US-10-724-972A-6352 (1-335) x US-08-781-986A-604 (1-2115)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Human Genome Sciences, STREET: 9410 Key West Avenue CITY: ROCYVILLE STATE: Maryland COUNTRY: USA
                 Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 604, Application US/10329624 Publication No. US20040043037A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gil H. Choi
Patrick S. Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Charles Kunsch
                   19.76%
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US-10-329-624-604
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                     Query Match:
DB:
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254 GluThrLeuSerGlnValAsnProGluArgMetPheIleMetThrAsn---LysAlaSer 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   292 AlaValLysAsnGlnArgValAspIleLeuAspArgAspLeuTrpAlaArgSerArgGly 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2556, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
                                                                                                                                                                                                                                                                                                                          194 MetAspLysAsnGlnLysValLeuProAlaValAlaAlaLysSerGlyLeuLeuAlaHis 213
                                                                                                                                                                                                                                                                                                                                                214 ProSerAsnSerTyrValGlydInPheLeuSerGInLeuGlyPheLysGluAlaLeuSer 233
                                                                                                                                                                                                                                                                                                                                                                                                                             234 AspAspValThrLysGlyLeuSerLysTyrLeuLysGlyProTyrLeuGlnMetAsnThr 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             273 SerAsnGluProSerLeuLysGluLeuGluLysAspPro---ValTrpLysLysLeuAsn 291
                                                                                                                                                                                                                                                                     GlylvstyskrgleuGluGluHisAspLysLysIleGluGluTyrLysLysGluIleThr 193
                                                                                                                                                                                         TyrAsnGluAsnIleAspAlapheLysThrIleSerLysAlaLeuGlyLysGluGluGlu
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Length:
Matches:
Conservative:
Mismatches:
Indels:
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18-10-/24-9/2a-6352.rnpb
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110 GinproAsnieuGluGluIleSeriysieuiysProAspLeuIleIleAlaAspAsnAsn 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-724-972A-6352 (1-335) x US-10-329-624-2556 (1-242)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative:
Mismatches:
Indels:
Gaps:
                 ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                            CURRENT APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION NUMBER: 08/956,171
APPLICATION NUMBER: 08/956,171
FILING DATE: Cactober 20, 1997
APPLICATION NUMBER: 08/96,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: MARK J. HYMAN
REGISTRATION NUMBER: 46,789
TELECOMMUNICATION NUMBER: 46,789
TELECOMMUNICATION NUMBER: 96,789
TELECOMMUNICATION NUMBER: 96,789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NO: 2556:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
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Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: ANDO, SEIKO
APPLICANT: ANDO, SEIKO
APPLICANT: ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID US-10-329-624-2556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 242 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 2556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.86e-20
333.00
90.00%
82.50%
CORRESPONDENCE ADDRESS
                                                                STATE: Maryland
COUNTRY: USA
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Best Local Similarity:
Query Match:
DB:
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Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlnProAsnLeuGluGluIleSerLysLeuLysProAspLeuIleIleAlaAspAsnAsn 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 ArgHisLysGlylleTyrLysAspLeuAsnLysIleAlaProThrlleGluLeuLysSer 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER RADABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33

OPERATION SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A

FILING DATE:
CLASSIFICATION 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: BASH

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REFERENCE/DOCKET NUMBER: PB248PP
TELECHMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512

INFORMATION FOR SEQ ID NO: 2556:
SEQUENCE CHARACTERISTICS:
CLENGTH: 242 base pairs
TYPE: NUMBER: ATTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
   ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 33
US-10-329-624-2556
; Sequence 2556, Application US/10329624
; Publication No. US20040043037A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Partick S. Dillon
Patrick S. Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.86e-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  333.00
90.00%
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19.70%
                                                  STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-781-986A-2556
                                                                                     ZIP: 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores
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DB:
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290 LeuAsnAlaValLysAsnGlnArgValAspIleLeuAspArgAspLeuTrpAlaArgSer 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 AsnSer---SerLysGluSerSerLysAspGlyValGluIleLysHisGluGluGlyThr 51
                                                                                             -----GACCTGGGGGAACGTGATTGGAATGAGTAC-----TCCATGATGGAGCTA 726
                                                                                                                             252 AsnThrGluThrLeuSerGlnValAsnProGluArgMetPhe-----IleMetThrAsn 269
                                                                                                                                                270 LysalaSerSerAsnGluProSerLeuLysGluLeuGluLysAspProValTrpLysLys 289
                                                                                                                                                                                                                 891
212 AlaHisProSerAsnSerTyrValGlyGlnPheLeuSerGlnLeuGlyPheLysGluAla
                                                                                                                                                                                                                                                                                            832 TCACCAGCAGTTCGGCAAGGTAGAACTTACGAGTTTGAAGACGAAACCTGGATGGTCGGC
                                                              232 LeuSerAgpAspValThrLysGlyLeuSerLysTyrLeuLysGlyProTyrLeuGlnMet
                            634 TATGGTCCC---GAGACCTTCTCTGGTTCAGTTCTGGAACAAGTTGGATTT-----
                                                                                                                                                                                                                                                                                                                              310 ArgGlyLeuIleSerSerGluGluMetAlaLysGluLeuValGlu 324
                                                                                                                                                                                                                                                                                                                                                  3309400
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
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APPLICANT: ANDO, SEIKO
APPLICANT: ANDO, SEIKO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: SENOH, AKIHIRO
APPLICANT: SENOH, AKINIRO
APPLICANT: OCAKI, AKI
ITIERE PERENCE: 249-125
CURRENT APPLICATION NUMBER: 105/97/38,626
CURRENT APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 2000-12-16
PRIOR FILING DATE: 2000-40-7
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
SOFTWARE: PATCHIN VET. 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09738626; Publication No. US20020197605A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIZGGUCHI, HIROSHI
ANDO, SEIKO
HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
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331.00
49.21%
28.57%
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAATCAATCCAACCTGAAGTTGCCAGCACTGGATATTCAGTGGAGCACGCAATGGGCACC 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ThrLysValProLysHisProLysArgValValValLeuGluTyrSerPheValAspAla 71
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514 GATGAGATGGACAAACTGATGTCAGACTTGGACACCCGTGCCACAGAGGTTGGTGAAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
                                          APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT PILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN Ver. 3.0
SEQ ID NO 375
LENGTH: 945
                                                                                                                                                                                                                                                                                                                            TYPE: DNA
) ORGANISM: Corynebacterium glutamicum
US-09-738-626-375
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331.00
49.21%
28.57%
19.59%
             YOKOI, HARUHIAN
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
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Best Local Similarity:
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                                  APPLICANT:
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Pred. No.:
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352795 GAATCCAACCTGAAGTTGCCAGCACTGGATATTCAGTGGAGCACGCAATGGGCACC 352854
                                                        353155 ACAAACTGGAATGAACAGGCAGAA-----ATCACTGCGGGCAGCAGTAAACAAGTCT 353205
                                                                                                                                                                                                                                                                            GAGGCTATTTATGATCAGCTTTCAGACATCGCACCAACCGTGATGTCCGAGGTTCCGGC 353154
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                                                                                                                                                92 IleLysProcedargAspLysIleGlyLysTyrThrServalGlyThrArgLysGlnPro 111
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                                       ThrLysValProLysHisProLysArgValValValLeuGluTyrSerPheValAspAla
                                                                                            LeuValala LeuAspValLysProValGlyIleAlaAspAspAsnLysLysAsnArgIle
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; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; TITLE OF INVENTION: Expression
; TITLE OF INVENTION: Expression
; TURENT APPLICATION UNMBER: US/09/974,300
; CURRENT APPLICATION NUMBER: US/09/974,300
; CURRENT PAPLICATION NUMBER: 09/680,598
; PRIOR APPLICATION NUMBER: 09/680,598
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US-09-974-300-2087
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63 ValLeuGluTyrSerPheValAspAlaLeuValAlaLeuAspValLysBroValGly11e 82
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147 GTACTCACGAATGAAGCGACAGAAGCGGTCTCGCACTTGGCGTAAAACCTGTCGGCGCC 206
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GTTCAATCCTGGCTGGGAGATCCATGGTATGACCATATTAAAGATAAAATGAAAGGCGTA 266
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387 CCGACCGTATTTGCCGAGACATTGTCAGGGGAATGGAAAACAAC-----TTTAAG 437
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558 GTCCGCTTTACAGATGCTGATACCCGCATCTATCACAAAGGATCATTTGCCGGAACGATT
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Matches:
Conservative:
Mismatches:
Indels:
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US-10-282-122A-17083
US-10-282-122A-17083
Sequence 17083, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Amudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FASLEEQ for Windows Version 4.
IENGTH: 648
TYPE: DNA
ORANISM: Bacillus licheniformis
                                                                                                                                     ; ORGANISM: Bacillus licheniformis
US-09-974-300-2087
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329.00
55.34%
35.92%
19.47%
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Sequence 351, Application US/10721922A

Sequence 351, Application US/10721922A

Publication No. US20050191732A1

GENERAL INFORMATION:
APPLICANT: Pompejus, Markus
APPLICANT: Except. Burkhard
APPLICANT: Alartwig
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APPLICANT: Alartwig
APPLICANTON NUMBER: US/10/721,922A
CURRENT APPLICATION NUMBER: US/602124
PRIOR FILING DATE: 2000-02-23
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US/60/141031
PRIOR FILING DATE: 1999-07-14
PRIOR FILING DATE: 1999-07-14
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932124.8
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932126.4
PRIOR PILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
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                                                                                                                                                                                                                                                                                                                                                           205 AlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPheLeuSer 224
313 AAAGAACCAGATTTAGAAGGTATAAAGTCGGCAAATCCAGATTTAATTATAATA---AAT 369
                                                129 AsnarqHisLysGly1leTyrLysAspLeuAsnLysIleAlaProThrileGluLeuLys 148
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                                                                                         370 GGAAGACAAGATTTTTATGAGCAATTGTCAAAAATAGCACCAACAATAAGTACAAGT
                                                                                                                                          149 SerPheAspGlyAspTyrAsnGlu------AsnIleAspAlaPheLysThrIle
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                                                                                                                                                                                                         TION: Identification of Essential Genes in Microorganisms
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APPLICANT: Trawick, John
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APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamanoco, Robert
APPLICANT: You, H.
APPLICANT: Xu, H.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essentis
TITLE OF INVENTION: Identification of Essentis
FILE REFERENCE: ELITRA, 034A
CURRENT PELLING DATE: 2003-02-20
PRIOR PELLING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PELLOATION NUMBER: 60/200, 727
PRIOR APPLICATION NUMBER: 60/200, 727
PRIOR PILING DATE: 2000-05-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
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                          Ohlsen, Kari
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2127.2 2133.7 removed icum	Length: Matches Conserv Mismetc Indels: Gaps:	x US-10-721-922A-351 -eAlaThrAlaAlaCyGGJyA : ::::: : : CTTCTAAGCTCCTGTTCTT	alGluI] :: \TTCAGI	lLeuGl :::::	.aAspAs ::: :GGAATC	rServa ATCTGT	ullell GATCAT	oThril :: AACCGD	FThrileSerLyBAlaLeuGlyLyBGluGluGluGlyLyB 	BLYBIl	aValAla ATTCCG	uSerGlı	rteuty
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APPLICATION NUMBER:) FILING DATE: 1999-07 APPLICATION NUMBER:) FILING DATE: 1999-07 ING DATE: 1999-07 OF SEQ ID NOS: 480 NO 351 NO 351 DNA ISM: Corynebacterium KEY: CDS INFORMATION: RXA0206-922A-351	••	2 (1-3 hevalt 3CGTCG	luSerS -	(BProL)	allysP:	PLYBI] ::::: CGAGCT	rLysLe : : : : : : : :	pLeuAs :: GCTTTC	GluAsnIleAsp GAACAGGCAGAA	gLeuGl ::: GATCTC	nGlnLy AACCGC	rTyrva :::: Crrcrc	rLysGl
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                                                                                                                                    163 ThrileSerLysAlaLeuGlyLysGluGluGluGlyLygeLysArgLeuGluGluHisAsp 182
292 ACCGCTGTCGGCGAAAAATGGAGCCGAACCTGGAGAAAATCCTTGAGCTGAAACCGGAT 351
                                      LeuileileAlaAspAsnAsnArgHisLysGlyIleTyrLysAspLeuAsnLysIleAla 142
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352 GTCATCCTGGCTTCAACGAAATTTCCTGATAAAGTGGTGAAAAAACTGGGTAACATCGCG 411
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1 Sequence 2107, Application US/09015242

2 Sequence 2107, Application US/09015242

3 Sequence 2107, Application US/09015242

3 SENERAL INPORMATION:

APPLICANT: Haselbeck, Robert

APPLICANT: Tranick, John D.

APPLICANT: Tranick, John D.

APPLICANT: Tranick, John D.

APPLICANT: Tranick, John D.

APPLICANT: Tranick, John D.

APPLICANT: Tranick, John D.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: 10011A

CURRENT APPLICATION NUMBER: 00/09-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR PILING DATE: 2000-05-25

PRIOR FILING DATE: 2000-05-26

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PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SEQ ID NO 2107
LENGTH: 321
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